

bond, and cyclising the octapeptide by reacting the specified side-chain residues with a difunctional linker to produce two amide bonds. The constrained helical peptides are used to treat or prevent HIV infection, especially as vaccines that generate antibodies that prevent viral membrane fusion or infectivity. Vaccines may contain constrained helical peptides derived from several different strains of HIV. The antibodies are also useful for diagnosing HIV infection. Other uses for the constrained helical peptides are in affinity purification of ligands (particularly where complete binding protein is not readily available, e.g. replacements for protein A in immunoglobulin purification); as epitope mimics for antibody production; for isolation of synthetic antibody clones from phage display libraries, or as stable forms of "floppy" peptides or proteins.

SQ Sequence 269 AA;

Query Match 100.0%; Score 139; DB 2; Length 269;
 Best Local Similarity 100.0%; Pred. No. 9 2e-11;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AVGMIGAMFLGFLGAAGSTNGATSMALTY 29
 Db 42 AVGMIGAMFLGFLGAAGSTNGATSMALTY 70

RESULT 3

ABU57711 standard; protein; 269 AA.

ID ABU57711;
 XX AC AC
 XX DT 10-APR-2003 (first entry)
 DE DB Human immunodeficiency virus (HIV) envelope protein gp41 #23.
 XX XX Human immunodeficiency virus; HIV; vaccine; helical peptide compound; viral membrane fusion; haptens; immunogen; peptidomimetic; gp41; envelope protein.
 XX XX Human immunodeficiency virus.
 OS XX US2002151473-A1.
 PN XX 17-OCT-2002.
 PD XX 15-MAY-2001; 2001US-00854816.
 XX XX 06-NOV-1996; 96US-00743658.
 PF XX 16-JUN-1997; 97US-0049787P.
 PR XX 16-JUN-1997; 97US-00876658.
 PR XX 05-NOV-1997; 97US-00965056.
 PA (BRAISTED AC.) BRAISTED A. C.
 PA (JUDICE J. K.) JUDICE J. K.
 PA (MCDOWELL R. S.) MCDOWELL R. S.
 PA (PHELAN J. C.) PHELAN J. C.
 PA (STAR M. A.) STAROVASNIK M. A.
 PA (WELLS J. A.) WELLS J. A.
 XX PI Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA,
 XX PI Wells JA;
 XX DR WPI; 2003-182525/18.

WPI; 2002-487624/52.
 XX New cyclic peptides from human immune deficiency virus gp41, useful for treatment or prevention of HIV infection, are constrained to have alpha-helical conformation.

XX Disclosure; Col 173-176; 17pp; English.
 CC The invention relates to cyclic peptides (A) with a constrained helical conformation, derived from gp41 (glycoprotein 41, a viral envelope protein) protein of human immunodeficiency virus (HIV). The cyclic peptides have formulas given in the specification part of which are derived from a consensus sequence of gp41 derived from HIV clades A, B, C, D, E or O. The peptides are used to cause induction of a specific immune response, resulting in antibodies that prevent virus-induced membrane fusion. The peptides are used to treat subjects with, or at risk

CC of, HIV infection, either as antifusion/anti-infection agents or, CC preferably where associated with a carrier, as an immunogen (including as CC vaccine) to raise antibodies. The antibodies may be used for diagnosis or CC prevention/treatment of HIV infection (i.e. acquired immunodeficiency CC syndrome, AIDS), e.g. prevention of mother-to-child transmission or in CC cases of health care accidents. The peptides can be based on specific HIV CC strains, e.g. breakthrough isolates of HIV that have developed during CC vaccine trials, so a combination of them should cover a wide range of CC protection. The present sequence is gp41 protein from a particular HIV CC clade used to derive a consensus sequence of gp41. (Updated on 29-AUG- CC 2003 to standardise OS field)

XX SQ Sequence 269 AA;

Query Match 100.0%; Score 139; DB 5; Length 269;
 Best Local Similarity 100.0%; Pred. No. 9.2e-11;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVGMIGAMFLGFLGAAGSTNGATSMALTY 29
 Db 42 AVGMIGAMFLGFLGAAGSTNGATSMALTY 70

RESULT 3

ABU57711 standard; protein; 269 AA.

ID ABU57711;

XX DT 10-APR-2003 (first entry)

DE DB Human immunodeficiency virus (HIV) envelope protein gp41 #23.

XX XX Human immunodeficiency virus; HIV; vaccine; helical peptide compound; viral membrane fusion; haptens; immunogen; peptidomimetic; gp41; envelope protein.

XX XX Human immunodeficiency virus.

OS XX US2002151473-A1.

PN XX 17-OCT-2002.

PD XX 15-MAY-2001; 2001US-00854816.

XX XX 06-NOV-1996; 96US-00743658.

PF XX 16-JUN-1997; 97US-0049787P.

PR XX 16-JUN-1997; 97US-00876658.

PR XX 05-NOV-1997; 97US-00965056.

PA (BRAISTED AC.) BRAISTED A. C.

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PA (PHELAN J. C.) PHELAN J. C.

PA (STAR M. A.) STAROVASNIK M. A.

PA (WELLS J. A.) WELLS J. A.

XX PI Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA,
 XX PI Wells JA;
 XX DR WPI; 2003-182525/18.

PS Novel constrained helical peptide compound useful for prophylactically or
 PT therapeutically treating mammal at risk for or infected with human
 XX immunodeficiency virus.

PS Disclosure; Fig 16; 180pp; English.

XX The invention describes a constrained helical peptide compound (I)
 CC comprising a first constrained helical peptide comprising a sequence of 8
 CC amino acids (a-as) having a first and second terminal residue both
 CC flanking an internal sequence of 6 a-as, where the terminal residues have
 CC a side chain that are linked to each other forming a locking group to

form a constrained helical peptide. (I) is useful for preparing antibodies that prevent viral membrane fusion, as happens, preferably attached to a carrier, for use as an immunogen to raise antibodies that have a diagnostic use, as a vaccine for treatment of patients at risk of or infected with HIV, to create combinatorial constrained helical peptide libraries that are useful in chemical selection systems, to isolate the binding determinants from alpha-helical binding domains of known proteins, for determining whether a binding determinant in an alpha-helical binding domain of a known protein can serve as a structural model for the design of peptidomimetics, to replace intact binding proteins or protein binding domains in the affinity purification of ligands, to mimic epitopes in proteins to selectively raise polyclonal or monoclonal antibodies against such individual epitopes for isolating synthetic antibody clones with a selected binding activity from phage display combinatorial libraries, to provide conformationally stable variants of peptides or proteins which exhibit floppy or unstable alpha-helical secondary structure at one or more sites in unrestrained form under conditions of interest. This is the amino acid sequence of an HIV envelope protein gp120, fragments of which are used in the creation of locked helix peptides

XX Sequence 269 AA;

Query Match 100.0%; Score 139; DB 6; Length 269;

Best Local Similarity 100.0%; Pred. No. 9.2e-11;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ AAW44250 standard; protein; 649 AA.

AC AAW44250;

XX DT 17-OCT-2003 (revised)

XX DT 26-JUN-1998 (first entry)

DE HIV-1 gp160 residues 33-681.

XX KW Vaccine; antibody; antigen; hydrophobic proteosome; pathogen; KW immune response; sexually transmitted disease; HIV; infection.

XX OS Human immunodeficiency virus 1.

XX Key Location/Qualifiers
FH 491. 519
FT /note= "hydrophobic region"

XX PN WO9801558-A2.

XX PD 15-JAN-1998.

XX PF 10-JUL-1997; 97WO-US012253.

XX PR 10-JUL-1996; 96US-0021687P.

XX DR 1998-110231/10.

XX PI Lowell GH, Vancott TC, Brix DL;

XX DR WPI: 1998-041353/04.

XX Vaccine compositions for eliciting neutralising antibodies - comprising PT antigen containing hydrophobic sequence or having added hydrophobic PT material, complexed to proteosomes or bio-adhesive nano-emulsions.

XX Claim 9; Page 22; 62pp; English.

XX

The present sequence represents HIV-1 gp160 residues 33-681 (the full protein is on the SWISS-PROT database Seq ID: 119434) used in a vaccine of the present invention. The vaccine composition is capable of eliciting neutralising antibodies in a subject to a pathogenic organism which antibodies are present in vaginal secretions, intestinal secretions, lung secretions or faeces. The vaccine comprises: (a) an antigen comprising a protein or peptide having: (i) an endogenous hydrophobic sequence of 3-50 non-polar or uncharged amino acids; (ii) added to the protein or peptide, an exogenous hydrophobic material comprising a fatty acyl group, or (iii) both polar or uncharged amino acids or a 8-18C fatty acid group, or (iv) both comprising proteosomes, bioadhesive nano-emulsions or both, where the complexed or coupled protein or peptide maintains a native structure of antigenic epitopes such that, upon administration to the subject, the antigen induces neutralising antibodies in one or more of vaginal, intestinal secretions, lung secretions and faeces, capable of neutralising the pathogenic organism. The compositions can be used for inducing an immune response against a pathogenic organism such as a causative agent of a sexually-transmitted or mucosally-transmitted disease, e.g. HIV infection. The compositions preserve the antigenicity of the protein or peptide epitopes while at the same time enhancing their immunogenicity. (Updated on 17-OCT-2003 to standardise OS field)

XX SQ Sequence 649 AA;

Query Match 100.0%; Score 139; DB 2; Length 649;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 491 AVGMGAMFLGFLGAGSTMGATSMALTV 519
Sequence 649 AA.

RESULT 5

AAW44250 standard; peptide; 865 AA.
ID AAW44250
AC AAW44250;

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AAW44250;

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AAW44250;

CC immunodeficiency virus type I (HIV-1) isolates. These proteins are used in a novel method for purifying HIV gp120 so as to provide a purified gp120 glycoprotein having protein/protein binding properties substantially identical to natural viral HIV gp120. The method involves fractionating a crude gp120 preparation containing full-length, glycosylated gp120 using ion exchange chromatography so as to provide a first collection of fractions. A fraction from the first collection is selected that exhibits specific binding affinity for CD4 peptide, thereby producing a first fractionated material. The first fractionated material is fractionated by hydrophobic interaction chromatography so as to provide a second collection of fractions from which a second collection is selected that exhibits specific binding affinity for CCR4 peptide. This second fraction is fractionated by size exclusion chromatography so as to provide a third collection of fractions exhibiting specific binding affinity for CD4 peptide, thereby providing the purified gp120. The purified gp120 can be used for antibody production and in vaccines. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 865 AA;

Query Match 100.0%; Score 139; DB 2; Length 865;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVGMI GAMFLGIGLGAAGSTMGATSMALTY 29
Db 521 AVGMI GAMFLGIGLGAAGSTMGATSMALTY 549

RESULT 6

ABPP73114 ABPP73114 standard; protein; 669 AA.
XX AC ABPP73114;
XX DT 17-JUN-2003 (first entry)
XX DB Amino acid sequence of a HIV-1 envelope protein mutant gp140.

XX Envelope glycoprotein; HIV-1; isolate 133; vaccine; HIV infection; 912;
KW gp140.
XX OS Synthetic.
XX Human immunodeficiency virus 1.
XX PN WO2003020755-A1.
XX PD 13-MAR-2003.
XX PP 06-SEP-2002; 2002WO-FR003039.
XX PR 06-SEP-2001; 2001FR-00011699.
XX PA (INMR) BIOMERIEUX SA.

XX PI Bedin F, Reynard F, Verrier B, Ataman-Oenal Y;
XX DR WPI; 2003-278759/27.
XX PT New mutated env gene of human immune deficiency virus; useful for genetic vaccination, also derived polypeptides having asparagine replaced by glutamine.
XX PS Claim 20; Page 99-102; 127pp; French.

XX CC The present sequence represents a truncated variant, designated gp140, of the Human immunodeficiency virus type 1 (HIV-1) isolate 133 envelope glycoprotein mutant g12 (see ACC43018 and ABP73115). The specification describes mutated HIV-1 envelope glycoproteins that have at least two mutations at glycosylation sites, conserved among primary isolates, each consisting of replacement of AAC or AAT (for Asn) by CAG or CAA (for Gln). The mutated envelope glycoprotein polymers and polypeptides are used in vaccines for prevention and treatment of HIV infection
XX SQ Sequence 669 AA;

Query Match 94.2%; Score 131; DB 6; Length 669;
Best Local Similarity 93.1%; Pred. No. 2.9e-09;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMI GAMFLGIGLGAAGSTMGATSMALTY 29
Db 499 AVGMI GAMFLGIGLGAAGSTMGATSMALTY 527

RESULT 8
ABPP73122 ABPP73122 standard; protein; 669 AA.
ID ABPP73122

XX PR 06-SEP-2001; 2001FR-00011699.
 XX PA
 XX (INMR) BIOMERIEUX SA.
 XX PI
 DE XX Bedin F, Reynard F, Verrier B, Ataman-Oenal Y;
 XX DR WPI; 2003-278759/27.
 XX N-PSDB; ACC43033.
 XX PT New mutated env gene of human immune deficiency virus, useful for genetic vaccination, also derived polypeptides having asparagine replaced by glutamine.
 PT XX Claim 12; Page 108-110; 127pp; French.
 PT XX PS
 XX CC The present sequence represents a truncated variant, designated gp140, of the Human immunodeficiency virus type 1 (HIV-1) isolate 133 envelope glycoprotein mutant g14 (see ACC43021 and ABP73118). The specification describes mutated HIV-1 envelope glycoproteins that have at least two mutations at glycosylation sites, conserved among primary isolates, each consisting of replacement of AAC or AAT (for Asn) by CAG or CAA (for Gln). The mutated envelope glycoprotein poly nucleotides and polypeptides are used in vaccines for prevention and treatment of HIV infection.
 CC XX Sequence 669 AA;
 CC SQ Query Match 94.2%; Score 131; DB 6; Length 669;
 CC Best Local Similarity 93.1%; Pred. No. 2.9e-09;
 CC Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 CC PT
 CC PR
 CC XX Qy 1 AVGMLGAMFLGFLGAAGSTMGATSMALTYV 29
 CC PA 499 AVGMUGAMFLGFLGAAGSTMGAASLALTV 527
 CC XX Db
 CC ID ABP73115 standard; protein; 844 AA.
 CC XX RESULT 10
 CC ID ABP73115
 CC AC ABP73115;
 CC XX DT 17-JUN-2003 (first entry)
 CC DE Amino acid sequence of HIV-1 envelope protein mutant g112.
 CC XX Envelope glycoprotein; HIV-1; isolate 133; vaccine; HIV infection; g112.
 CC OS Synthetic.
 CC OS Human immunodeficiency virus 1.
 CC XX PN WO2003020755-A1.
 CC XX PD 13-MAR-2003.
 CC XX PF 06-SEP-2002; 2002WO-FR001039.
 CC XX PR 06-SEP-2001; 2001FR-00011699.
 CC XX PT (INMR) BIOMERIEUX SA.
 CC DE XX Bedin F, Reynard F, Verrier B, Ataman-Oenal Y;
 CC DR WPI; 2003-278759/27.
 CC N-PSDB; ACC43038.
 CC PT New mutated env gene of human immune deficiency virus, useful for genetic vaccination, also derived polypeptides having asparagine replaced by glutamine.
 CC XX Claim 20; Page 94-97; 127pp; French.
 CC XX PS
 CC XX PD
 CC XX PF 06-SEP-2002; 2002WO-FR003039.
 CC XX PT
 CC XX The present sequence represents the Human immunodeficiency virus type 1

CC (HIV-1) isolate 133 envelope glycoprotein mutant g112. The specification
 CC describes mutated HIV-1 envelope glycoproteins that have at least two
 CC mutations at glycosylation sites, conserved among primary isolates, each
 CC consisting of replacement of AAC or AAT (for Asn) by CAG or CAA (for
 CC Gln). The mutated envelope glycoprotein polymucleotides and polypeptides
 CC are used in vaccines for prevention and treatment of HIV infection
 XX Sequence 844 AA;

Query Match 94.2%; Score 131; DB 6; Length 844;
 Best Local Similarity 93.1%; Pred. No. 3.7e-09; Indels 0; Gaps 0;
 Matches 27; Conservative 1; Mismatches 1; DT 17-JUN-2003 (first entry)
 XX

Qy 1 AVGMIGAMFLGFLGAGSTNGATSMALTV 29
 Db 499 AVGMIGAMFLGFLGAGSTNGATSMALTV 527

RESULT 11
 ID ABP73112 standard; protein: 844 AA.
 XX

AC ABP73112;

XX DT 17-JUN-2003 (first entry)

DE Amino acid sequence of HIV-1 envelope protein mutant g112.

XX KW Envelope glycoprotein; HIV-1; isolate 133; vaccine; HIV infection; g112.

XX OS Synthetic.

OS Human immunodeficiency virus 1.

XX SQ WO2003020755-A1.

XX PD 13-MAR-2003.

XX PR 06-SEP-2002; 2002WO-FR003039.

XX PF 06-SEP-2001; 2001FR-00011699.

XX PA (INMR) BIOMERIEUX SA.

PI Bedin F, Reynard F, Verrier B, Ataman-Oenal Y;

XX DR WPI; 2003-278759/27.

XX N-PSDB; ACC43021.

XX PT New mutated env gene of human immune deficiency virus, useful for genetic vaccination, also derived polypeptides having asparagine replaced by glutamine.

XX PT Sequence 844 AA;

XX PS Claim 12; Page 102-103; 127pp; French.

XX The present sequence represents the Human immunodeficiency virus type 1 (HIV-1) isolate 133 envelope glycoproteins that have at least two mutations at glycosylation sites, conserved among primary isolates, each consisting of replacement of AAC or AAT (for Asn) by CAG or CAA (for Gln). The mutated envelope glycoprotein polymucleotides and polypeptides are used in vaccines for prevention and treatment of HIV infection

XX SQ Sequence 844 AA;

XX DR Query Match 94.2%; Score 131; DB 6; Length 844;

XX Best Local Similarity 93.1%; Pred. No. 3.7e-09; Indels 1; Gaps 0; Matches 27; Conservative 1; Mismatches 1; DT 17-JUN-2003 (first entry)

XX OS Amino acid sequence of a HIV-1 envelope protein mutant.

XX KW Envelope glycoprotein; HIV-1; vaccine; HIV infection.

XX PA Synthetic.

OS Human immunodeficiency virus 1.

XX SQ WO2003020755-A1.

XX PD 13-MAR-2003.

XX The present sequence represents the Human immunodeficiency virus type 1 (HIV-1) isolate 133 envelope glycoproteins that have at least two mutations at glycosylation sites, conserved among primary isolates, each consisting of replacement of AAC or AAT (for Asn) by CAG or CAA (for Gln). The mutated envelope glycoprotein polymucleotides and polypeptides are used in vaccines for prevention and treatment of HIV infection

XX SQ Sequence 844 AA;

XX DR Query Match 94.2%; Score 131; DB 6; Length 844;

XX Best Local Similarity 93.1%; Pred. No. 3.7e-09; Indels 1; Gaps 0; Matches 27; Conservative 1; Mismatches 1; DT 17-JUN-2003 (first entry)

XX OS Amino acid sequence of a HIV-1 envelope protein mutant.

XX KW Envelope glycoprotein; HIV-1; vaccine; HIV infection.

XX PA Synthetic.

OS Human immunodeficiency virus 1.

XX SQ WO2003020755-A1.

XX PD 13-MAR-2003.

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Job time : 12.7198 secs

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GenCore version 5.1.7
OM protein - protein search, using sw model
Run on: March 7, 2006, 17:45:48 ; Search time 2.22419 Seconds
(without alignments) 1254.519 Million cell updates/sec

Title: US-09-938-406-1_COPY_523_551
Perfect score: 139
Sequence: 1 AVGMGLGAGSTMGATSMALTV 29
Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	139	100.0	868	1	VCLJH4		env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)
2	91.4	861	1	VCLJSC			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
3	89.2	69	2	S60706			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
4	88.5	69	2	S60690			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
5	87.8	358	2	S70417			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
6	87.8	358	2	S22000			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
7	87.8	358	2	S22002			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
8	86.3	855	1	VCLJA2			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
9	85.6	856	1	VCLJ3W			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
10	83.5	69	2	S60689			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
11	82.0	69	2	S60691			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
12	81.7	294	2	S60525			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
13	80.2	68	2	S60693			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
14	79.5	854	2	S13288			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
15	79.5	859	2	S101672			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
16	78.8	357	2	S22004			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
17	78.8	357	2	S22006			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
18	78.8	851	2	S33985			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
19	78.8	853	2	S54384			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
20	78.8	855	1	VCLJZ2			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
21	78.8	856	1	VCLJH3			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
22	78.8	856	1	VCLJVL			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
23	78.1	68	2	S60696			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
24	78.1	301	2	S60532			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
25	78.1	301	2	S60531			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
26	78.1	357	2	S21994			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
27	78.1	445	2	A41621			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
28	78.1	847	2	T09448			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1
29	78.1	847	2	S13289			env polyprotein - env polyprotein precursor - human immunodeficiency virus type 1, HIV-1

ALIGNMENTS

RESULT 1

VCLJH4

env polyprotein - human immunodeficiency virus type 1 (isolate CDC-451)

N;Alternate names: coat protein gp41
N;Contains: coat protein gp120; coat protein gp41
C;Species: human immunodeficiency virus type 1, HIV-1
C;Accession: C25523
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
R;Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare, S.
Proc. Natl. Acad. Sci. U.S.A. 83: 8380-8384, 1986
A;Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human immunodeficiency virus type 1
A;Reference number: A94136; MUID:87041461; PMID:3490666
A;Accession: C25523
A;Molecule type: DNA
A;Residues: 1-868 <DES>
A;Cross-references: UNIPROT:P05879; UNIPARC:UPI00012A014; GB:M13137; NID:9326460; PIDN:14459

C;Genetics:

A;Gene: env

C;Superfamily: type B retrovirus env polyprotein

C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protein
P;1-521/Product: coat protein gp120 #status predicted <GP1>
F;522-866/Product: coat protein gp245 #status predicted <GP2>
F;89,138,139,142,166,198,208,245,252,273,287,300,312,342,349,365,371,395,405,409,459,

Query Match Score: 100.0%; Score: 139; DB: 1; Length: 868;
Best Local Similarity: 100.0%; Pred. No.: 2e-10;
Matches: 29; Conservative: 0; Missmatches: 0; Indels: 0; Gaps: 0;

QY 1 AVGMLGAMFLGFIAAGSTMGATSMALTV 29
Db 523 AVGMGLGAGSTMGATSMALTV 551

RESULT 2

VCLJSC

env polyprotein precursor - human immunodeficiency virus type 1, HIV-1

N;Alternate names: coat protein gp41
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1980 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C;Accession: B28922
R;Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta
Virology 164, 531-536, 1988
A;Title: Envelope sequences of two new United States HIV-1 isolates
A;Reference number: A28922; MUID:88219542; PMID:3365091
A;Molecule type: DNA
A;Residues: 1-861 <GUR>
A;Cross-references: UNIPARC:UPI000174A39
C;Genetics:
A;Gene: env
C;Superfamily: type B retrovirus env polyprotein

C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protein
 F;1-29/Domain: signal sequence #status Predicted <SIG>
 F;30-861/Product: env polyprotein #status Predicted <SPPP>
 F;87-129,135-140,143,159,163,187-198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match Score 127; DB 1; Length 861;
 Best Local Similarity 91.4%; Pred. No. 7.1e-09;
 Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVGMIGAMFLGFLGAGSTMGATSMALTY 29
 Db 516 AVGTGAMFLGFLGAGSTMGATSMALTY 544

RESULT 3

S60706 env protein - human immunodeficiency virus type 1 (isolate 88) (fragment)
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
 R;Accession: S60706
 R;Rojas, J.M.; Dopazo, J.; Najera, I.; Sanchez-Palomino, S.; Olivares, I.; Martin, M.J.;
 Virus Res. 31, 331-342, 1994
 A;Title: Molecular epidemiology of HIV-1 in Madrid.
 A;Reference number: S60687; MUID:94249284; PMID:7545926
 A;Status: preliminary; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-69 <RO>
 A;Cross-references: UNIPROT:Q76161; UNIPARC:UPI000010624B; EMBL:Z29688; NID:9808997; PID:
 C;Superfamily: type E retrovirus env polyprotein

Query Match Score 124; DB 2; Length 69;
 Best Local Similarity 89.2%; Pred. No. 1.5e-09;
 Matches 25; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMIGAMFLGFLGAGSTMGATSMALTY 29
 Db 8 AVGLVGMFLGFLGAGSTMGATSMALTY 36

RESULT 4

S61690 env protein - human immunodeficiency virus type 1 (isolate 2080) (fragment)
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
 R;Rojas, J.M.; Dopazo, J.; Najera, I.; Sanchez-Palomino, S.; Olivares, I.; Martin, M.J.;
 Virus Res. 31, 331-342, 1994
 A;Title: Molecular epidemiology of HIV-1 in Madrid.
 A;Reference number: S60687; MUID:94249284; PMID:7545926
 A;Accession: S60690
 A;Status: preliminary; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-69 <RO>
 A;Cross-references: UNIPROT:Q76153; UNIPARC:UPI0000101115; EMBL:Z29692; NID:98089981; PID:
 C;Superfamily: type E retrovirus env polyprotein

Query Match Score 123; DB 2; Length 69;
 Best Local Similarity 88.5%; Pred. No. 2e-09;
 Matches 25; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVGMIGAMFLGFLGAGSTMGATSMALTY 29
 Db 8 AVGMIGAMFLGFLGAGSTMGATSMALTY 36

RESULT 5

S70417 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment)
 C;Species: human immunodeficiency virus type 1, HIV-1
 A;Variety: patient 3B
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C;Accession: S70417

R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992
 A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by sequencing gp120/gp41
 A;Reference number: S70417; MUID:92144209; PMID:1736940

A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-358 <STE1>
 A;Cross-references: UNIPROT:Q78140; UNIPARC:UPI0000008E84C; EMBL:X61351; NID:960184; PIDN:
 C;Superfamily: type E retrovirus env polyprotein

Query Match Score 122; DB 2; Length 358;
 Best Local Similarity 86.2%; Pred. No. 1.4e-08;
 Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AVGMIGAMFLGFLGAGSTMGATSMALTY 29
 Db 13 AVGTGAMFLGFLGAGSTMGATSMALTY 41

RESULT 6

S22000 envelope protein gp120/gp41 - human immunodeficiency virus type 1
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 R;Accession: S22000
 R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
 submitted to the EMBL Data Library, July 1991
 A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by sequencing gp120/gp41
 A;Reference number: S21990
 A;Accession: S22000
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-358 <STE1>
 C;Superfamily: type E retrovirus env polyprotein

Query Match Score 122; DB 2; Length 358;
 Best Local Similarity 86.2%; Pred. No. 1.4e-08;
 Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AVGMIGAMFLGFLGAGSTMGATSMALTY 29
 Db 13 AVGTGAMFLGFLGAGSTMGATSMALTY 41

RESULT 7

S22002 envelope protein gp120/gp41 - human immunodeficiency virus type 1, HIV-1
 C;Species: isolate 3U
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 R;Accession: S22002; S70418
 R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
 submitted to the EMBL Data Library, July 1991
 A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by sequencing gp120/gp41
 A;Reference number: S21990
 A;Accession: S22002
 A;Molecule type: DNA
 A;Residues: 1-358 <STE1>
 A;Cross-references: UNIPROT:Q78141; UNIPARC:UPI0000178609; EMBL:X61352; NID:960186; PIDN:
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992
 A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by sequencing gp120/gp41
 A;Reference number: S70417; MUID:92144209; PMID:1736940

Query Match Score 122; DB 2; Length 358;

A;Accession: S60527
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-294 <JAW>
A;Cross-references: UNIPARC:UPI0000102742; EMBL:X72029; NID:9468633; PIDN:CAA50912.1; PI
A;Experimental source: isolate CI-13-4
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; glycoprotein; immunodeficiency; polyprotein

Query Match 81.7%; Score 113.5; DB 2; Length 294;
Best Local Similarity 86.2%; Pred. No. 1.4e-07; Indels 1; Gaps 1;
Matches 25; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 1 AVGMLGAMFLGFLGAAGSTMGATSMALTY 29
Db 237 AIG-LGAMFLGFLGAAGSTMGAASTMILTY 264

RESULT 13

S60693 env protein - human immunodeficiency virus type 1 (isolate 306) (fragment)

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C;Accession: S60693 R;O'Rojas, J.M.; Dopazo, J.; Najera, I.; Sanchez-Palomino, S.; Olivares, I.; Martin, M.J.;

Virus Res., 31, 331-342, 1994

A;Title: Molecular epidemiology of HIV-1 in Madrid.

A;Reference number: S60687; PMID:7545926

A;Accession: S60693 A;Status: preliminary; translation not shown

A;Molecule type: DNA
A;Residues: 1-68 <ROJ>

A;Cross-references: UNIPROT:Q76157; UNIPARC:UPI000010B1F0; EMBL:Z29684; NID:9808989; PID

C;Superfamily: type E retrovirus env polyprotein

Query Match 80.2%; Score 111.5; DB 2; Length 68;
Best Local Similarity 86.2%; Pred. No. 6.3e-08; Indels 1; Gaps 1;
Matches 25; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 1 AVGMLGAMFLGFLGAAGSTMGATSMALTY 29
Db 8 AVG-IGAMFLGFLGAAGSTMGARSMLTY 35

RESULT 14

S13288 env protein - human immunodeficiency virus type 1, HIV-1

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Dec-2004

C;Accession: S13288 R;O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.

A;Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120

A;Reference number: S13288; PMID:9103044; PMID:2172833

A;Accession: S13288 A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-854 <OBR>

A;Cross-references: UNIPROT:Q85582; UNIPROT:Q72502; UNIPROT:O90178; UNIPROT:Q78243; UNIF

Query Match 79.5%; Score 110.5; DB 2; Length 854;
Best Local Similarity 82.8%; Pred. No. 1e-06; Indels 1; Gaps 1;
Matches 24; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 AVGMLGAMFLGFLGAAGSTMGATSMALTY 29
Db 510 AVG-IGALFLGFLGAAGSTMGCTSMILTY 537

RESULT 15

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OM protein - protein search, using sw model

Run on: March 7, 2006, 17:40:55 ; Search time 13:30:24 Seconds

(without alignment(s)/sec
1538.097 Million cell updates/secTitle: US-09-938-406-1_COPY_523_551
Perfect score: 139
Sequence: 1 AVGMGLGAGTSMGATSMALTV 29Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:

2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries.Database : UniProt_05.80:
1: uniprot_sprot:
2: uniprot_trembl:
* * *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	139	100.0	868	1	ENV HIV1C4	P0579	P0579 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [1]
2	132	95.0	877	2	Q6IUG0_9HIV1	Q6IUG0 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
3	132	95.0	877	2	Q6IUG1_9HIV1	Q6IUG1 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
4	131	95.0	877	2	Q6IUG2_9HIV1	Q6IUG2 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
5	131	94.2	799	2	Q6IUL1_9HIV1	Q6IUL1 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
6	131	94.2	814	2	Q6QLK5_9HIV1	Q6QLK5 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
7	131	94.2	844	2	Q6M6L1_9HIV1	Q6M6L1 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
8	131	94.2	844	2	Q6OLK7_9HIV1	Q6OLK7 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
9	131	94.2	844	2	Q6QLK8_9HIV1	Q6QLK8 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
10	131	94.2	844	2	Q6QLK9_9HIV1	Q6QLK9 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
11	131	94.2	844	2	Q6OLL0_9HIV1	Q6OLL0 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
12	131	94.2	859	2	Q6QLJ4_9HIV1	Q6QLJ4 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
13	131	94.2	859	2	Q6QLJ5_9HIV1	Q6QLJ5 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
14	131	94.2	859	2	Q6QLJ6_9HIV1	Q6QLJ6 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
15	131	94.2	859	2	Q6QLJ7_9HIV1	Q6QLJ7 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
16	131	94.2	859	2	Q6QLJ8_9HIV1	Q6QLJ8 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
17	131	94.2	859	2	Q6QLJ9_9HIV1	Q6QLJ9 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
18	131	94.2	859	2	Q6QLK0_9HIV1	Q6QLK0 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
19	131	94.2	859	2	Q6QLK1_9HIV1	Q6QLK1 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
20	131	94.2	859	2	Q6QLK2_9HIV1	Q6QLK2 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
21	131	94.2	859	2	Q6QLK3_9HIV1	Q6QLK3 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
22	131	94.2	859	2	Q6QLK4_9HIV1	Q6QLK4 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
23	131	94.2	859	2	Q6QLK6_9HIV1	Q6QLK6 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
24	131	94.2	868	2	Q6QLL3_9HIV1	Q6QLL3 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
25	130	93.5	858	2	Q7SUT2_9HIV1	Q7SUT2 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
26	130	93.5	859	2	P87924_9HIV1	P87924 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
27	130	93.5	859	2	Q7SUT4_9HIV1	Q7SUT4 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
28	130	93.5	859	2	Q7SUT6_9HIV1	Q7SUT6 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
29	130	93.5	859	2	Q7SUT8_9HIV1	Q7SUT8 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	
30	130	93.5	859	2	Q7SUT9_9HIV1	Q7SUT9 human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). [2]	

Scoring table: BL0SUM62	Gapop 10.0 , Gapext 0.5	2166443 seqs, 705528306 residues	Total number of hits satisfying chosen parameters:	2166443
Minimum DB seq length: 0	Maximum DB seq length: 2000000000			
Post-processing: Minimum Match 0%	Maximum Match 100%			

RESULT 1
ENV HIV1C4
ID ENV HIV1C4
AC P0579;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
DE Name=ENV;
GN HIV-1.
OS Human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1).
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentiviruses; Primate lentivirus group.
OX NCBI_TaxID=11687;

ALIGNMENTS

ENV HIV1C4	STANDARD;	PRT;	868 AA.
AC P0579;			
DT 01-NOV-1988 (Rel. 09, Created)			
DT 01-NOV-1988 (Rel. 09, Last sequence update)			
DT 13-SEP-2005 (Rel. 48, Last annotation update)			
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
DE Name=ENV;			
GN HIV-1.			
OS Human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1).			
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;			
OC Lentiviruses; Primate lentivirus group.			
OX NCBI_TaxID=11687;			
RN NUCLEOTIDE SEQUENCE OF 34-43.			
RX MEDLINE=97044461; PubMed=34906666;			
RA Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A., Andersen P.R., Devare S.G.;			
RT "Molecular cloning and primary nucleotide sequence analysis of a distinct human immunodeficiency virus isolate reveal significant divergence in its genomic sequences". Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).			
RL RT			
RN PROTEIN SEQUENCE OF 34-43.			
RX MEDLINE=90255924; PubMed=2187500;			
RA Deivko A.L., Copeland T., Oroszlan S., Gallo R.C., Sangerdharan M.G.;			
RA Devico A.L., Copeland T., Oroszlan S., Gallo R.C., Sangerdharan M.G.;			
RT "Characterization of the secreted, native gp120 and gp160 of the human immunodeficiency virus type 1." AIDS Res. Hum. Retroviruses 6:371-380(1990).			
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CC CC			
DR PIR: C25523; VLTH4.			
DR HSSP; P19549; IMEQ.			
DR SMR; P05879; 84-128, 87-212, 206-503, 552-638.			
DR HIV-M13137; ENVS/CD45.			
DR InterPro; IPR00777; GP120.			
DR Pfam; PF0516; GP120; 1.			
DR Pfam; PF0511; GP11; 1.			
KW AIDS; Capsid Protein; Direct protein sequencing; Glycoprotein; Polypeptide; Signal; Structural protein; Transmembrane.			
KW SIGNAL	1	33	
FT CHAIN	34	522	Exterior membrane glycoprotein.
FT CHAIN	523	868	Transmembrane glycoprotein.
FT CAREOHD	89	89	N-linked (GlcNAc. . .) (Potential).
FT CAREOHD	131	131	N-linked (GlcNAc. . .) (Potential).

[1]	NUCLEOTIDE SEQUENCE RP Gorry P.R., Kristman K.J., Morgan T., Moore J.P., Mascola J.R., RA Agopian K., Holm H., Mehle A., Taylor J., Farzan M., Wang H., RA Ellery P., Willey S., Clapham P., Wollinsky S.M., Crowe S.M., RA Gabuzda D.; SUBMITTED [MAY-2004] to the EMBL/GenBank/DDJB databases. EMBL:AY624304; AAC:AT44417.1; -; Genomic_c_DNA. HSSP: P04578; 1K33. DR Q6QK5; Q6QK5_9HIV1 PRELIMINARY; PRT; 814 AA. ID Q6QK5_9HIV1 PRELIMINARY; AC Q6QK5; DT 05-JUL-2004 (TREMBrel); 27, Created DT 05-JUL-2004 (TREMBrel); 27, Last sequence update DE Envelope glycoprotein. Name=env; Name=env; Human immunodeficiency virus 1. Viruses; Retroviridae; Lentivirus; Primate lentivirus group. NCBI_TaxID=11676; RN [1] RP NUCLEOTIDE SEQUENCE. RC STRAIN=133; RX PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004; RA Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.; RT "Evolutionary Dynamics of the Glycan Shield of the Human Immunodeficiency Virus Envelope during Natural Infection and Implications for Exposure of the G12 Epitope."; RL J. Virol. 78:12625-12637(2004). DR EMBL: AV35434; AAC:AS58777; 1; Genomic_RNA. DR SMR: Q6QK5; 200-94; 543-629. DR GO: 0042028; C:host cell nucleus; IEA. DR GO: 0019031; C:viral envelope; IEA. DR GO: 0005198; P:structural molecule activity; IEA. DR InterPro: IPR000328; Env.GP1. DR InterPro: IPR00777; GP20. DR InterPro: IPR000625; REV_protein. PFam: PF00516; GP120; 1. PFam: PF00517; GPAP1; 1. PFam: PF00424; REV; 1. DR Envelope protein. SQ SEQUENCE: 814 AA; 91785 MW; 8AAB45F6CA6953A1 CRC64; Query Match 95.0%; Score 132; DB 2; Length 877; Best Local Similarity 93.1%; Pred. No. 1.6e-08; Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Db 532 AVGMIGAMEFLGFLGAGSTMGAAASLALT 560
[1]	NUCLEOTIDE SEQUENCE RN Q6QK5_9HIV1 PRELIMINARY; ID Q6QK5_9HIV1 PRELIMINARY; AC Q6QK5; DT 05-JUL-2004 (TREMBrel); 27, Created DT 05-JUL-2004 (TREMBrel); 27, Last sequence update DB Envelope glycoprotein. Name=env; Name=env; Human immunodeficiency virus 1. Viruses; Retroviridae; Lentivirus; Primate lentivirus group. NCBI_TaxID=11676; RN [1] RP NUCLEOTIDE SEQUENCE. RC STRAIN=133; RX PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004; RA Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.; RT "Evolutionary Dynamics of the Glycan Shield of the Human Immunodeficiency Virus Envelope during Natural Infection and Implications for Exposure of the G12 Epitope."; RL J. Virol. 78:12625-12637(2004). DR EMBL: AV35434; AAC:AS58777; 1; Genomic_RNA. DR SMR: Q6QK5; 200-94; 543-629. DR GO: 0042028; C:host cell nucleus; IEA. DR GO: 0019031; C:viral envelope; IEA. DR GO: 0005198; P:structural molecule activity; IEA. DR GO: 0003700; P:transcription factor activity; IEA. DR InterPro: IPR000328; Env.GP1. DR InterPro: IPR00777; GP20. DR InterPro: IPR000625; REV_protein. PFam: PF00516; GP120; 1. PFam: PF00517; GPAP1; 1. PFam: PF00424; REV; 1. DR Envelope protein. SQ SEQUENCE: 814 AA; 91785 MW; 8AAB45F6CA6953A1 CRC64; Query Match 94.2%; Score 131; DB 2; Length 799; Best Local Similarity 93.1%; Pred. No. 2e-08; Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Db 514 AVGMIGAMEFLGFLGAGSTMGAAASLALT RESULT 7 Q6QK5_9HIV1 PRELIMINARY; ID Q6QK5_9HIV1 PRELIMINARY; AC Q6QK5_9HIV1 PRELIMINARY; DT 01-JUN-1998 (TREMBrel); 06, Created DT 01-JUN-1998 (TREMBrel); 06, Last sequence update DE Envelope glycoprotein. Name=env; Name=env; Human immunodeficiency virus 1. Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae; OC Lentivirus; Primate lentivirus group. NCBI_TaxID=11676; RN [1] RP NUCLEOTIDE SEQUENCE. RX MEDLINE=99372987; PubMed=10445815; DOI=10.1089/0889229310548; RA Ataman-Onal Y., Coiffier C., Giraud A., Babic-Erceg A., Biron F.; RA Verrier B.; RT "Comparison of complete env gene sequences from individuals with symomatic primary HIV type 1 infection."; RL AIDS Res. Hum. Retroviruses 15:1035-1039(1999). DR EMBL: AF041126; AAC:02517.1; -; Genomic_DNA. DR HSSP: P04578; 1K34.
[1]	NUCLEOTIDE SEQUENCE SQ SEQUENCE: 799 AA; 89998 MW; A42EF332C626DB65 CRC64; Query Match 94.2%; Score 131; DB 2; Length 799; Best Local Similarity 93.1%; Pred. No. 2e-08; Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Db 1 AVGMIGAMEFLGFLGAGSTMGAAASLALT 29

DR SMR; 055561; 140-479, 528-614.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP1; 1.
 AIDS: Envelope protein; Transmembrane.
 SQ SEQUENCE 844 AA; 95831 MW; CA255D577DE418A8 CRC64;
 Query Match 94.2%; Score 131.; DB 2; Length 844;
 Best Local Similarity 93.1%; Pred. No. 2.1e-08;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 AVGMIGAMPLGFLGAAGSTMGATSMALTY 29
 Db 499 AVGMIGAMPLGFLGAAGSTMGATSMALTY 527

RESULT 8
 Q6QIK7_9HIV1 PRELIMINARY; PRT; 844 AA.
 ID Q6QIK7_9HIV1 PRELIMINARY; PRT; 844 AA.
 AC DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Envelope glycoprotein.
 Name=env;
 OS Human immunodeficiency virus 1.
 Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 Lentivirus; Primate lentivirus group.
 NCBI_TaxID=11676;

[1]
 RN NUCLEOTIDE SEQUENCE.
 STRAIN=133;
 PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;
 RA Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.,
 RT "Evolutionary Dynamics of the Glycan Shield of the Human
 Immunodeficiency Virus Envelope during Natural Infection and
 Implications for Exposure of the 2G12 Epitope.",
 RL J. Virol. 78:12625-12637 (2004).
 EMBL; AY535432; AAS58775; 1; -; Genomic_RNA.
 SNR; Q6QIK7; 140-479, 528-614.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR Pfam; PF00517; GP120; 1.
 AIDS: Envelope protein; Transmembrane.
 SQ SEQUENCE 844 AA; 95748 MW; 9C52688JAD476D16D CRC64;

Query Match 94.2%; Score 131.; DB 2; Length 844;
 Best Local Similarity 93.1%; Pred. No. 2.1e-08;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 AVGMIGAMPLGFLGAAGSTMGATSMALTY 29
 Db 499 AVGMIGAMPLGFLGAAGSTMGATSMALTY 527

RESULT 9
 Q6QIK8_9HIV1 PRELIMINARY; PRT; 844 AA.
 ID Q6QIK8_9HIV1 PRELIMINARY; PRT; 844 AA.
 AC DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DE Envelope glycoprotein.
 Name=env;
 OS Human immunodeficiency virus 1.

OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Lentivirus; Primate lentivirus group.
 OC NCBITaxID=11676;
 RN NUCLEOTIDE SEQUENCE.
 STRAIN=133;
 PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;
 RA Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.,
 RT "Evolutionary Dynamics of the Glycan Shield of the Human
 Immunodeficiency Virus Envelope during Natural Infection and
 Implications for Exposure of the 2G12 Epitope.",
 RL J. Virol. 78:12625-12637 (2004).
 EMBL; AY535430; AAS58773; 1; -; Genomic_RNA.
 SNR; Q6QIK8; 140-479, 528-614.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR Pfam; PF00517; GP120; 1.
 AIDS: Envelope protein; Transmembrane.
 SQ SEQUENCE 844 AA; 95761 MW; 5CEFA0FOFB03C58 CRC64;

Query Match 94.2%; Score 131.; DB 2; Length 844;
 Best Local Similarity 93.1%; Pred. No. 2.1e-08;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 AVGMIGAMPLGFLGAAGSTMGATSMALTY 29

Db	499 AVGMIGAMFLGFLGAAGSTMGAASLLTV 527	DR InterPro; IPR000328; Env GP41. DR InterPro; IPR000777; GP120. DR Pfam; PF00516; GP120; 1. AIDS; Envelope protein; Transmembrane.
RESULT 11	Q6QLJ0_9HIV1 PRELIMINARY;	PRT; 844 AA.
ID	Q6QLJ0 ;	
AC	Q6QLJ0 ;	
DT	05-JUL-2004 (TREMBLrel. 27, Created)	
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)	
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)	
DB	Envelope glycoprotein.	
GN	Name=env;	
OS	Human immunodeficiency virus 1.	
OC	Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;	
OC	Lentivirus; Primate lentivirus group.	
OX	NCBI_TaxID=11676;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=133;	
RX	PubMed=1507649; DOI=10.1128/JVI.78.22.12625-12637.2004;	
RA	Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verzier B., Barin F.;	
RT	"Evolutionary Dynamics of the Glycan Shield of the Human Immunodeficiency Virus Envelope during Natural Infection and Implications for Exposure of the 2G12 Epitope.";	
RT	J. Virol. 78:12625-12637(2004).	
RL	EMBL:AY335429; AAS8772.1; -; Genomic_RNA.	
DR	SMR; Q6QLJ0; 140-479, 528-614.	
DR	GO:0016021; C:integral to membrane; IEA.	
DR	GO:0019031; C:viral envelope; IEA.	
DR	GO:0005198; F:structural molecule activity; IEA.	
InterPro	IPI000328; Env GP41.	
InterPro	IPI000777; GP120.	
PFam	PF00516; GP120; 1.	
DR	PF00517; GP41; 1.	
DR	Q6QLJ0 ;	
KW	AIDS; Envelope protein; Transmembrane.	
SEQUENCE	844 AA; 95807 MW; 17A31D1BD9CFOADC CRC64;	
Query Match	94.2%; Score 131; DB 2; Length 844;	
Best Local Similarity	93.1%; Pred. No. 2.1e-08;	
Matches	27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Score	1 AVGMIGAMFLGFLGAAGSTMGAASLLTV 29	
Db	499 AVGMIGAMFLGFLGAAGSTMGAASLLTV 527	
RESULT 12	Q6QLJ4_9HIV1 PRELIMINARY;	PRT; 859 AA.
ID	Q6QLJ4 ;	
AC	Q6QLJ4 ;	
DT	05-JUL-2004 (TREMBLrel. 27, Created)	
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)	
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)	
DE	Envelope glycoprotein.	
GN	Name=env;	
OS	Human immunodeficiency virus 1.	
OC	Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;	
OC	Lentivirus; Primate lentivirus group.	
OX	NCBI_TaxID=11676;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=133;	
RX	PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;	
RA	Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verzier B., Barin F.;	
RT	"Evolutionary Dynamics of the Glycan Shield of the Human Immunodeficiency Virus Envelope during Natural Infection and Implications for Exposure of the 2G12 Epitope.";	
RT	J. Virol. 78:12625-12637(2004).	
RL	EMBL:AY53445; AAS58788.1; Genomic_RNA.	
DR	SMR; Q6QLJ5; 200-494, 543-629.	
DR	GO:0016021; C:integral to membrane; IEA.	
DR	GO:0019031; C:viral envelope; IEA.	
DR	GO:0005198; F:structural molecule activity; IEA.	
DR	InterPro; IPI000328; Env GP41.	
DR	InterPro; IPI000777; GP120.	
DR	PFam; PF00516; GP120; 1.	
DR	Pfam; PF00517; GP120; 1.	
KW	AIDS; Envelope protein; Transmembrane.	
SEQUENCE	859 AA; 97398 MW; 8378D387EA019CD2 CRC64;	
Query Match	94.2%; Score 131; DB 2; Length 859;	
Best Local Similarity	93.1%; Pred. No. 2.1e-08;	
Matches	27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Score	1 AVGMIGAMFLGFLGAAGSTMGAASLLTV 29	
Db	514 AVGMIGAMFLGFLGAAGSTMGAASLLTV 542	
RESULT 13	Q6QLJ5_9HIV1 PRELIMINARY;	PRT; 859 AA.
ID	Q6QLJ5_9HIV1 PRELIMINARY;	
AC	Q6QLJ5_9HIV1 PRELIMINARY;	
DT	05-JUL-2004 (TREMBLrel. 27, Created)	
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)	
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)	
DE	Envelope glycoprotein.	
GN	Name=env;	
OS	Human immunodeficiency virus 1.	
OC	Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;	
OC	Lentivirus; Primate lentivirus group.	
OX	NCBI_TaxID=11676;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=133;	
RX	PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;	
RA	Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verzier B., Barin F.;	
RT	"Evolutionary Dynamics of the Glycan Shield of the Human Immunodeficiency Virus Envelope during Natural Infection and Implications for Exposure of the 2G12 Epitope.";	
RT	J. Virol. 78:12625-12637(2004).	
RL	EMBL:AY53446; AAS58789.1; Genomic_RNA.	
DR	SMR; Q6QLJ4; 200-494, 543-629.	
DR	GO:0016021; C:integral to membrane; IEA.	
DR	GO:0019031; C:viral envelope; IEA.	
DR	GO:0005198; F:structural molecule activity; IEA.	

RP NUCLEOTIDE SEQUENCE.
 STRAIN=133;
 RX PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;
 RA Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.;
 RT "Evolutionary Dynamics of the Glycan Shield of the Human
 Immunodeficiency Virus Envelope during Natural Infection and
 Implications for Exposure of the G12 Epitope.",;
 RT J. Virol. 78:12625-12637 (2004).
 DR EMBL: AY535444; ASN58797.1; Genomic_RNA.
 DR SNR: Q6QJ76; 543-529.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0019031; C:viral envelope; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR InterPro: IPR000348; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Envelope protein; Transmembrane.
 SQ SEQUENCE 859 AA; 97581 MW; CDFF3D4.98277012B CRC64;

Query Match 94.2%; Score 131; DB 2; Length 859;
 Best Local Similarity 93.1%; Pred. No. 2.e-08;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Name=env;

Qy 1 AVGMIGAMFLGFLGAAGSTMGATSMALTY 29
 Db 514 AVGMIGAMFLGFLGAAGSTMGASLALTY 542

RESULT 15
 Q6QJ7 9HIV1
 ID Q6QJ7 9HIV1 PRELIMINARY;
 AC Q6QJ7;
 DT 05-JUL-2004 (TREMBrel. 27, Created)
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)
 DE Envelope glycoprotein.
 GN Human immunodeficiency virus 1.
 OS Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Lentivirus; Primate lentivirus group.
 OX NCBI_TaxID:11676;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 STRAIN=133;
 RX PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;
 RA Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.;
 RT "Evolutionary Dynamics of the Glycan Shield of the Human
 Immunodeficiency Virus Envelope during Natural Infection and
 Implications for Exposure of the G12 Epitope.",;
 RT J. Virol. 78:12625-12637 (2004).
 DR EMBL: AY535442; ASN58785.1; Genomic_RNA.
 DR SNR: Q6QJ7; 200-543; 543-629.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0019031; C:viral envelope; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR InterPro: IPR000348; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP41; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Envelope protein; Transmembrane.
 SQ SEQUENCE 859 AA; 97483 MW; 5B54B76DSF4245A8 CRC64;

Query Match 94.2%; Score 131; DB 2; Length 859;
 Best Local Similarity 93.1%; Pred. No. 2.e-08;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Name=env;

Qy 1 AVGMIGAMFLGFLGAAGSTMGATSMALTY 29
 Db 514 AVGMIGAMFLGFLGAAGSTMGASLALTY 542

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OM protein - protein search, using sw model

Run on: March 7, 2006, 17:51:03 ; Search time 3.03687 Seconds
('without alignments')
789.495 Million cell updates/sec

Title: US-09-938-406-1_COPY_523_551

Perfect score: 139

Sequence: 1 AVGMGLGFLGIAAGSTMGATSMALTV 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 4 summaries

Database : Issued_Patents_AA:
1: /cgn2_6/prodata/1/iaa/5_COMB.pep:
2: /cgn2_6/prodata/1/iaa/6_COMB.pep:
3: /cgn2_6/prodata/1/iaa/H_COMB.pep:
4: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:
5: /cgn2_6/prodata/1/iaa/RE_COMB.pep:
6: /cgn2_6/prodata/1/iaa/backfiles1.pep:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	269	2 US-08-965-056-29	Sequence 29, App1
2	129	92.8	267	2 US-08-965-056-27	Sequence 27, App1
3	128	92.1	269	2 US-08-965-056-47	Sequence 47, App1
4	127	91.4	269	2 US-08-965-056-12	Sequence 12, App1
5	127	91.4	855	2 US-07-956-483-14	Sequence 14, App1
6	127	91.4	887	2 US-08-972-240-5	Sequence 5, App1
7	126	90.6	269	2 US-08-965-056-25	Sequence 25, App1
8	126	90.6	269	2 US-08-965-056-32	Sequence 32, App1
9	90.5	269	2 US-08-965-056-44	Sequence 44, App1	
10	125	89.9	269	2 US-08-965-056-21	Sequence 21, App1
11	124	89.2	79	2 US-08-965-056-58	Sequence 58, App1
12	124	89.2	269	2 US-08-965-056-36	Sequence 36, App1
13	124	89.2	269	2 US-08-965-056-43	Sequence 43, App1
14	124	89.2	269	2 US-08-965-056-46	Sequence 46, App1
15	123	88.5	269	2 US-08-965-056-31	Sequence 31, App1
16	123	88.5	269	2 US-08-965-056-42	Sequence 42, App1
17	122	87.8	269	2 US-08-965-056-42	Sequence 6, App1
18	122	87.8	269	2 US-08-965-056-23	Sequence 23, App1
19	122	87.8	269	2 US-08-965-056-24	Sequence 24, App1
20	121	87.1	105	2 US-08-965-056-52	Sequence 52, App1
21	121	87.1	105	2 US-08-965-056-54	Sequence 54, App1
22	120	86.3	40	2 US-08-982-3	Sequence 3, App1
23	120	86.3	40	2 US-09-948-2	Sequence 3, App1
24	120	86.3	40	2 US-09-977-534-3	Sequence 3, App1
25	120	86.3	269	2 US-08-965-056-28	Sequence 28, App1
26	120	86.3	269	2 US-08-965-056-30	Sequence 30, App1
27	120	86.3	269	2 US-08-965-056-76	Sequence 45, App1

ALIGNMENTS

RESULT 1
US-08-965-056-29
Sequence 29, Application US/08965056
; Patent No. 6271188

GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted
; Kevin Judge
; Robert S. McDowell
; J. Christopher Phelan
; Melissa A. Starovasnik

APPLICANT: James A. Wilts

TITLE OF INVENTION: Constrained Helical Peptides and Methods of
TITLE OF INVENTION: Making Same
NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/965,056
FILED DATE: 05-NOV-1998-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
INFORMATION FOR SEQ ID NO.: 29:
SEQUENCE CHARACTERISTICS:
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/955-9881
US-08-965-056-29

Query Match Score 139; DB 2;
Best Local Similarity 100.0%;
Matches 29; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 AVGMDAMFLGFLGAGSTMGATSMALTV 29

Db 42 AVGMLGAMFLGFLGAAGSTMGATSMALTV 70

RESULT 2

US-08-965-056-27

Sequence 27, Application US/08965056

Patent No. 6271198

GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

APPLICANT: J. Kevin Judge

APPLICANT: Robert S. McDowell

APPLICANT: J. Christopher Phelan

APPLICANT: Melissa A. Starovasnik

APPLICANT: James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/965,056

FILING DATE: 05-No. 6271198-1997

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Ph.D., Timothy E.

REGISTRATION NUMBER: P1005R2

REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 269 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

RESULT 4

US-08-965-056-12

Query Match Score 128;

Best Local Similarity 89.7%;

Pred. No. 1e-10;

Matches 26; Mismatches 1;

Indels 0;

Gaps 0;

; GENERAL INFORMATION:

Qy 1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29

Db 42 AVGVIGAMFLGFLGAAGSTMGATSMALTV 70

; ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Ph.D., Timothy E.

REGISTRATION NUMBER: P1005R2

REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-965-056-27

Query Match Score 129;

Best Local Similarity 93.1%;

Pred. No. 7.5e-11;

Matches 27; Mismatches 2;

Indels 0;

Gaps 0;

; GENERAL INFORMATION:

Qy 1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29

Db 42 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 70

; ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Ph.D., Timothy E.

REGISTRATION NUMBER: P1005R2

REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

RESULT 3

US-08-965-056-47

Sequence 47, Application US/08965056

Patent No. 6271198

GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

APPLICANT: J. Kevin Judge

APPLICANT: Robert S. McDowell

APPLICANT: J. Christopher Phelan

APPLICANT: Melissa A. Starovasnik

APPLICANT: James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/965,056

FILING DATE: 05-No. 6271198-1997

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Ph.D., Timothy E.

REGISTRATION NUMBER: P1005R2

REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/965,056
 FILING DATE: 05-Nov. 6271198-1997
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Torchia, Ph.D., Timothy E.
 REGISTRATION NUMBER: 36,700
 REFERENCE/DOCKET NUMBER: P1005R2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/925-8674
 TELEFAX: 650/932-9881
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 269 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-965-056-25

Query Match 90.6%; Score 126; DB 2; Length 269;
 Best Local Similarity 89.7%; Pred. No. 2.1e-10;
 Matches 26; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 8
 US-08-965-056-32
 ; Sequence 32, Application US/08965056
 ; Patent No. 6271198
 GENERAL INFORMATION:
 APPLICANT: Andrew C. Braisted
 APPLICANT: J. Kevin Judice
 APPLICANT: Robert S. McDowell
 APPLICANT: J. Christopher Phelan
 APPLICANT: Melissa A. Starovasnik
 APPLICANT: James A. Wells
 TITLE OF INVENTION: Constrained Helical Peptides and Methods of
 Making Same
 NUMBER OF SEQUENCES: 113

Qy 1 AVGMIGAMFLGFLGAGSTMGATSMALTY 29
 Db 42 AVGLGAVTFLGFLGAGSTMGATSMALTY 70

Query Match 90.6%; Score 126; DB 2; Length 269;
 Best Local Similarity 89.7%; Pred. No. 2.1e-10;
 Matches 26; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 9
 US-08-965-056-44
 ; Sequence 44, Application US/08965056
 ; Patent No. 6271198
 GENERAL INFORMATION:
 APPLICANT: Andrew C. Braisted
 APPLICANT: J. Kevin Judice
 APPLICANT: Robert S. McDowell
 APPLICANT: J. Christopher Phelan
 APPLICANT: Melissa A. Starovasnik
 APPLICANT: James A. Wells
 TITLE OF INVENTION: Constrained Helical Peptides and Methods of
 Making Same
 NUMBER OF SEQUENCES: 113

Qy 1 AVGMIGAMFLGFLGAGSTMGATSMALTY 29
 Db 42 AVGLGAVTFLGFLGAGSTMGATSMALTY 70

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/965,056
 FILING DATE: 05-No. 6271198-1997
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Torchia, Ph.D., Timothy E.
 REGISTRATION NUMBER: 36,700
 REFERENCE/DOCKET NUMBER: P1005R2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/925-8674
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 269 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-965-056-44

Query Match 90.6%; Score 126; DB 2; Length 269;
 Best Local Similarity 89.7%; Pred. No. 2.1e-10;
 Matches 26; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMIGAMFLGFLGAGSTMGATSMALTY 29
 Db 42 AVGLGAVTFLGFLGAGSTMGATSMALTY 70

RESULT 10
 US-08-965-056-21
 ; Sequence 21, Application US/08965056
 ; Patent No. 6271198
 GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted
 APPLICANT: J. Kevin Judge
 APPLICANT: Robert S. McDowell
 APPLICANT: J. Christopher Phelan
 APPLICANT: Melissa A. Starovashnik
 APPLICANT: James A. Wells
 TITLE OF INVENTION: Constrained Helical Peptides and Methods of
 NUMBER OF SEQUENCES: Making Same
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/965,056
 FILING DATE: 05-No 6271198-1997
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Torchia, PhD., Timothy E.
 REGISTRATION NUMBER: 36,700
 REFERENCE/DOCKET NUMBER: P1005R2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/9225-8674
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 58:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 79
 TOPOLOGY: 79 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-965-056-58

Query Match 89.2%; Score 124; DB 2; Length 79;
 Best Local Similarity 89.7%; Pred. No. 9.8e-11;
 Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 12
 US-08-965-056-36
 Sequence 36, Application US/08965056
 Patent No. 6271198
 GENERAL INFORMATION:
 APPLICANT: Andrew C. Braisted
 APPLICANT: J. Kevin Judge
 APPLICANT: Robert S. McDowell
 APPLICANT: J. Christopher Phelan
 APPLICANT: Melissa A. Starovashnik
 APPLICANT: James A. Wells
 TITLE OF INVENTION: Constrained Helical Peptides and Methods of
 SEQUENCE CHARACTERISTICS:
 LENGTH: 269 amino acids
 TOPOLOGY: Linear
 US-08-965-056-21

Query Match 89.9%; Score 125; DB 2; Length 269;
 Best Local Similarity 89.7%; Pred. No. 2.9e-10;
 Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Query 1 AVGMGAMPFLGFLGAAGSTMAGTSMALTY 29
 Db 42 AVGTGAMPFLGFLGAAGSTMAGAASVATV 70

RESULT 11
 US-08-965-056-58
 Sequence 58, Application US/08965056
 Patent No. 6271198
 GENERAL INFORMATION:
 APPLICANT: Andrew C. Braisted
 APPLICANT: J. Kevin Judge
 APPLICANT: Robert S. McDowell
 APPLICANT: J. Christopher Phelan
 APPLICANT: Melissa A. Starovashnik
 APPLICANT: James A. Wells
 TITLE OF INVENTION: Constrained Helical Peptides and Methods of
 NUMBER OF SEQUENCES: Making Same
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/965,056
 FILING DATE: 05-No 6271198-1997
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Torchia, PhD., Timothy E.
 REGISTRATION NUMBER: 36,700
 REFERENCE/DOCKET NUMBER: P1005R2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/9225-8674
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 269 amino acids
 TOPOLOGY: Linear
 US-08-965-056-36

Query Match 89.2%; Score 124; DB 2; Length 269;

Best Local Similarity 89.7%; Pred. No. 4e-10; Mismatches 1; Indels 2; Gaps 0;

Qy 1 AVGMGLGMLFLGFLGAAGSTMGAATSMALTV 29
 Db 42 AVGTIGLAMFLGFLGAAGSTMGAASVALTV 70

RESULT 13

US-08-965-056-43
 Sequence 43, Application US/08965056
 Patent No. 6271198
 GENERAL INFORMATION:
 APPLICANT: Andrew C. Braisted
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: Robert S. McDowell
 FILING DATE: 05-No. 6271198-1997
 CURRENT APPLICATION DATA:
 APPLICANT: J. Kevin Judice
 APPLICANT: J. Christopher Phelan
 APPLICANT: Melissa A. Starovasnik
 APPLICANT: James A. Wells
 TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
 NUMBER OF SEQUENCES: 113
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICANT: WinPatin (Genentech)
 APPLICATION NUMBER: US/08/965,056
 FILING DATE: 05-No. 6271198-1997
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Torchia, PhD., Timothy E.
 REGISTRATION NUMBER: P1005R2
 REFERENCE/DOCKET NUMBER: P1005R2
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Torchia, PhD., Timothy E.
 REGISTRATION NUMBER: P1005R2
 REFERENCE/DOCKET NUMBER: P1005R2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/952-8674
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:
 LENGTH: 269 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear

US-08-965-056-46

Query Match 89.2%; Score 124; DB 2; Length 269;

Best Local Similarity 89.7%; Pred. No. 4e-10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AVGMGLGMLFLGFLGAAGSTMGAATSMALTV 29
 Db 42 AVGTIGLAMFLGFLGAAGSTMGAASVALTV 70

RESULT 15

US-08-965-056-31
 Sequence 31, Application US/08965056
 Patent No. 6271198
 GENERAL INFORMATION:
 APPLICANT: Andrew C. Braisted
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: J. Kevin Judice
 APPLICANT: Robert S. McDowell
 APPLICANT: J. Christopher Phelan
 APPLICANT: Melissa A. Starovasnik
 APPLICANT: James A. Wells
 TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
 NUMBER OF SEQUENCES: 113
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICANT: WinPatin (Genentech)
 APPLICATION NUMBER: US/08/965,056
 FILING DATE: 05-No. 6271198-1997
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Torchia, PhD., Timothy E.

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
 NUMBER OF SEQUENCES: 113
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

Query Match 89.2%; Score 124; DB 2; Length 269;

Best Local Similarity 89.7%; Pred. No. 4e-10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AVGMGLGMLFLGFLGAAGSTMGAATSMALTV 29
 Db 42 AVGTIGLAMFLGFLGAAGSTMGAASVALTV 70

RESULT 14

US-08-965-056-46
 Sequence 46, Application US/08965056
 Patent No. 6271198
 GENERAL INFORMATION:
 APPLICANT: Andrew C. Braisted
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: J. Kevin Judice
 APPLICANT: Robert S. McDowell
 APPLICANT: J. Christopher Phelan
 APPLICANT: Melissa A. Starovasnik
 APPLICANT: James A. Wells
 TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
 NUMBER OF SEQUENCES: 113
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICANT: WinPatin (Genentech)
 APPLICATION NUMBER: US/08/965,056
 FILING DATE: 05-No. 6271198-1997
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Torchia, PhD., Timothy E.

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
 NUMBER OF SEQUENCES: 113
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

Query Match 89.2%; Score 124; DB 2; Length 269;

Best Local Similarity 89.7%; Pred. No. 4e-10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AVGMGLGMLFLGFLGAAGSTMGAATSMALTV 29
 Db 42 AVGTIGLAMFLGFLGAAGSTMGAASVALTV 70

REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/932-9881
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-965-056-31

Query Match Similarity 88.5%; Score 123; DB 2; Length 269;
Best Local Similarity 86.2%; Pred. No. 5.5e-10;
Matches 25; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AVGMIGAMFLGFLGAAGSTMGATSMALTY 29
Db 42 AVGIIGAMFLGFLGAAGSTMGARSMTLV 70

Search completed: March 7, 2006, 17:52:52
Job time : 4.03687 secs

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OM protein - protein search, using sw model

Run on: March 7, 2006, 17:51:52 ; Search time 9.4528 Seconds
(without alignments)
1281.847 Million cell updates/sec

Title: US-09-938-406-1_COPY_523_551

Perfect score: 139

Sequence: 1 AVGMGLAMFGLGAGSTMGATSMWLTIV 29

Scoring table: BL05062

Gapext: 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0‡

Maximum Match 100‡

Listing first 45 summaries

Database : Published Applications AA_Main:^{*}

1: /cgm2_6/podata/1/pubpaas/us07_pubcomb.pep:^{*}

2: /cgm2_6/podata/1/pubpaas/us08_pubcomb.pep:^{*}

3: /cgm2_6/podata/1/pubpaas/us09_pubcomb.pep:^{*}

4: /cgm2_6/podata/1/pubpaas/us10_pubcomb.pep:^{*}

5: /cgm2_6/podata/1/pubpaas/us10b_pubcomb.pep:^{*}

6: /cgm2_6/podata/1/pubpaas/us11_pubcomb.pep:^{*}

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
1	139	100.0	269	3 US-09-854-816-29	Sequence 29, App1
2	139	100.0	868	3 US-09-938-406-1	Sequence 1, App1
3	93.5	94.2	669	5 US-10-487-094-14	Sequence 17, App1
4	131	94.2	669	5 US-10-487-094-17	Sequence 20, App1
5	131	94.2	669	5 US-10-487-094-20	Sequence 25, App1
6	131	94.2	669	5 US-10-487-094-25	Sequence 11, App1
7	131	94.2	844	5 US-10-487-094-11	Sequence 12, App1
8	131	94.2	844	5 US-10-487-094-12	Sequence 15, App1
9	131	94.2	844	5 US-10-487-094-15	Sequence 18, App1
10	131	94.2	844	5 US-10-487-094-18	Sequence 24, App1
11	131	94.2	844	5 US-10-487-094-24	Sequence 2, App1
12	130	93.5	883	4 US-10-941-916-2	Sequence 2, App1
13	130	93.5	883	3 US-10-441-949-2	Sequence 2, App1
14	130	93.5	883	5 US-10-780-507-2	Sequence 121, App1
15	129	92.8	267	3 US-09-854-816-27	Sequence 27, App1
16	128	92.1	269	3 US-09-854-816-47	Sequence 47, App1
17	127	91.4	269	3 US-09-854-816-12	Sequence 12, App1
18	124	90.6	269	3 US-09-854-816-25	Sequence 25, App1
19	126	90.6	269	3 US-09-854-816-32	Sequence 32, App1
20	126	90.6	269	3 US-09-854-816-44	Sequence 44, App1
21	126	90.6	360	4 US-10-214-870-60	Sequence 60, App1
22	126	90.6	269	3 US-09-854-816-21	Sequence 21, App1
23	125	89.9	269	3 US-09-854-816-47	Sequence 58, App1
24	124	89.2	79	3 US-09-854-816-58	Sequence 36, App1
25	124	89.2	269	3 US-09-854-816-36	Sequence 43, App1
26	124	89.2	269	3 US-09-854-816-43	Sequence 46, App1
27	124	89.2	269	3 US-09-854-816-34	Sequence 28, App1

ALIGNMENTS

RESULT 1
US-09-854-816-29
; Sequence 29, Application US/09854816
; Patent No. US20090151473A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; J. Kevin Justice
; Robert S. McDowell
; J. Christopher Phelan
; Melissa A. Starovanski
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/854,816
; FILING DATE: 15-May-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; PRIORITY NUMBER: 08/965,056
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/552-9881
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
; US-09-854-816-29
; Score 139; DB 3; Length 269;
; Pred. No. 2.5e-10;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AVGMIGAMFLGFLGAAGSTMGATSMALTV 29
 Db 42 AVGMIGAMFLGFLGAAGSTMGATSMALTV 70

RESULT 2
 US-09-938-406-1
 Sequence 1, Application US/09938406
 Patent No. US20030155120A1
 GENERAL INFORMATION:
 APPLICANT: Lowell, George
 Vancott, Thomas
 Birx, Deborah
 TITLE OF INVENTION: PROTEIN AND PEPTIDE VACCINES FOR
 INDUCING MUCOSAL IMMUNITY
 FILE REFERENCE: 406-16-20002.10
 CURRENT APPLICATION NUMBER: US/09/938,406
 CURRENT FILING DATE: 2001-08-21
 PRIOR APPLICATION NUMBER: US 09/214,701
 PRIOR FILING DATE: 1999-09-30
 PRIOR APPLICATION NUMBER: PCT/US 97/12253
 PRIOR FILING DATE: 1997-07-10
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 868
 TYPE: PRT
 ORGANISM: Virus HIV-1
 US-09-938-406-1

Query Match 100.0%; Score 139; DB 3; Length 868;
 Best Local Similarity 100.0%; Prod. No. 8.6e-10
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AVGMIGAMFLGFLGAAGSTMGATSMALTV 29
 Db 523 AVGMIGAMFLGFLGAAGSTMGATSMALTV 551

RESULT 3
 US-10-487-094-14
 Sequence 14, Application US/10487094
 Publication No. US20050065320A1
 GENERAL INFORMATION:
 APPLICANT: BEDIN, Frederic
 REYNARD, Bernard
 VERRIER, Bernard
 APPLICANT: ATAMAN-ONAL, Yasemin
 TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
 FILE REFERENCE: 118745
 CURRENT APPLICATION NUMBER: US/10/487,094
 CURRENT FILING DATE: 2001-09-06
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 14
 LENGTH: 669
 TYPE: PRT
 ORGANISM: HIV-1 mutant g14
 US-10-487-094-14

Query Match 94.2%; Score 131; DB 5; Length 669;
 Best Local Similarity 93.1%; Prod. No. 7.4e-09
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 AVGMIGAMFLGFLGAAGSTMGATSMALTV 29
 Db 499 AVGMIGAMFLGFLGAAGSTMGATSMALTV 527

RESULT 6
 US-10-487-094-25
 Sequence 25, Application US/10487094
 Publication No. US20050065320A1
 GENERAL INFORMATION:
 APPLICANT: BEDIN, Frederic
 REYNARD, Frederic

APPLICANT: VERRIER, Bernard
 APPLICANT: ATAMAN-ONAL, Yasemin
 TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
 FILE REFERENCE: 118745
 CURRENT APPLICATION NUMBER: US/10/487,094
 CURRENT FILING DATE: 2004-02-19
 PRIOR APPLICATION NUMBER: FR 01/11699
 PRIOR FILING DATE: 2001-09-06
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 25
 LENGTH: 669
 TYPE: PRT
 ORGANISM: HIV-1 mutant 922
 US-10-487-094-15

Query Match 94.2%; Score 131; DB 5; Length 669;

Best Local Similarity 93.1%; Pred. No. 7.4e-09;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMLGAMPLGLGAAGSTMGATSMALTY 29
 Db 499 AVGMLGAMPLGLGAAGSTMGAAASLALTV 527

RESULT 7
 US-10-487-094-11
 Sequence 11, Application US/10487094
 Publication No. US20050065320A1
 GENERAL INFORMATION:
 APPLICANT: BEGIN, Frederic
 REYNARD, Frederic
 VERRIER, Bernard
 APPLICANT: ATAMAN-ONAL, Yasemin
 TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
 FILE REFERENCE: 118745
 CURRENT APPLICATION NUMBER: US/10/487,094
 CURRENT FILING DATE: 2004-02-19
 PRIOR APPLICATION NUMBER: FR 01/11699
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 11
 LENGTH: 844
 TYPE: PRT
 ORGANISM: HIV-1 mutant 9112
 US-10-487-094-11

Query Match 94.2%; Score 131; DB 5; Length 844;

Best Local Similarity 93.1%; Pred. No. 9.5e-09;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMLGAMPLGLGAAGSTMGATSMALTY 29
 Db 499 AVGMLGAMPLGLGAAGSTMGAAASLALTV 527

RESULT 8
 US-10-487-094-12
 Sequence 12, Application US/10487094
 Publication No. US20050065320A1
 GENERAL INFORMATION:
 APPLICANT: BEGIN, Frederic
 REYNARD, Bernard
 APPLICANT: VERRIER, Bernard
 APPLICANT: ATAMAN-ONAL, Yasemin
 TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
 FILE REFERENCE: 118745
 CURRENT APPLICATION NUMBER: US/10/487,094
 CURRENT FILING DATE: 2004-02-19
 PRIOR APPLICATION NUMBER: FR 01/11699
 NUMBER OF SEQ ID NOS: 26

Query Match 94.2%; Score 131; DB 5; Length 844;
 Best Local Similarity 93.1%; Pred. No. 9.5e-09;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMLGAMPLGLGAAGSTMGATSMALTY 29
 Db 499 AVGMLGAMPLGLGAAGSTMGAAASLALTV 527

RESULT 9
 US-10-487-094-15
 Sequence 15, Application US/10487094
 Publication No. US20050065320A1
 GENERAL INFORMATION:
 APPLICANT: BEGIN, Frederic
 REYNARD, Frederic
 VERRIER, Bernard
 APPLICANT: ATAMAN-ONAL, Yasemin
 TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
 FILE REFERENCE: 118745
 CURRENT APPLICATION NUMBER: US/10/487,094
 CURRENT FILING DATE: 2004-02-19
 PRIOR APPLICATION NUMBER: FR 01/11699
 PRIOR FILING DATE: 2001-09-06
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 18
 LENGTH: 844
 TYPE: PRT
 ORGANISM: HIV-1 mutant 914
 US-10-487-094-18

Query Match 94.2%; Score 131; DB 5; Length 844;
 Best Local Similarity 93.1%; Pred. No. 9.5e-09;

Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0; SEQ ID NO: 24

Query 1 AVGMIGAMFLGFLGAAGSTMGATSMALTY 29
Db 499 AVGMIGAMFLGFLGAAGSTMGAAASLALT 527

RESULT 11 US-10-487-094-24

; Sequence 24, Application US/10487094
; Publication No. US2005065320A1
; GENERAL INFORMATION:
; APPLICANT: BEDIN, Frederic
; APPLICANT: REYNARD, Frederic
; APPLICANT: VERTIER, Bernard
; TITLE OF INVENTION: ATAMAN-OVAL, Yasermin
; FILE REFERENCE: 118745
; CURRENT APPLICATION NUMBER: US/10/487,094
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: FR 01/11699
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 844
; TYPE: PRT
; ORGANISM: HIV-1 mutant 922

US-10-487-094-24

Query Match 94.2%; Score 131; DB 5; Length 844;
Best Local Similarity 93.1%; Pred. No. 9-0e-09
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query 1 AVGMIGAMFLGFLGAAGSTMGATSMALTY 29
Db 499 AVGMIGAMFLGFLGAAGSTMGAAASLALT 527

RESULT 12 US-10-441-926-2

; Sequence 2, Application US/10441926
; Publication No. US20040115621A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Allen
; APPLICANT: Ross, Howard A.
; APPLICANT: Mullins, James I.
; TITLE OF INVENTION: ANCESTRAL VIRUSES AND VACCINES
; FILE REFERENCE: 08937-011001
; CURRENT APPLICATION NUMBER: US/10/441,926
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2001-02-18
; PRIOR APPLICATION NUMBER: US 60/183,659
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially generated peptide

US-10-441-926-2

Query Match 93.5%; Score 130; DB 4; Length 883;
Best Local Similarity 93.1%; Pred. No. 1.4e-08
Matches 27; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Query 1 AVGMIGAMFLGFLGAAGSTMGATSMALTY 29
Db 538 AVGMIGAMFLGFLGAAGSTMGAAASMTLV 566

RESULT 13 US-10-441-949-2

; Sequence 2, Application US/10441949
; Publication No. US20040116684A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Allen
; APPLICANT: Ross, Howard A.
; APPLICANT: Mullins, James I.
; TITLE OF INVENTION: ANCESTRAL VIRUSES AND VACCINES
; FILE REFERENCE: 08937-012001
; CURRENT APPLICATION NUMBER: US/10/441,949
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 60/183,659
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially generated peptide

US-10-441-949-2

Query Match 93.5%; Score 130; DB 5; Length 883;
Best Local Similarity 93.1%; Pred. No. 1.4e-08
Matches 27; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 14 US-10-780-507-2

; Sequence 2, Application US/10780507
; Publication No. US20050137387A1
; GENERAL INFORMATION:
; APPLICANT: MULLINS, James I.
; APPLICANT: RODRIGO, Alien G.
; APPLICANT: LEARN, Gerald H.
; APPLICANT: LI, Fusheng
; APPLICANT: NICKLE, David C.
; APPLICANT: JENSEN, Mark A.
; TITLE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPOS
; FILE REFERENCE: 16336-001320US
; CURRENT APPLICATION NUMBER: US/10/780,507
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US 60/1204,204
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 60/183,659
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/447,586
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ancestral HIV-1 group M, subtype B, env sequence

US-10-780-507-2

Query Match 93.5%; Score 130; DB 5; Length 883;
Best Local Similarity 93.1%; Pred. No. 1.4e-08
Matches 27; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVGMIGAMFLGFLGAGSTMGATSMALTV 29
 Db 538 AVGMIGAMFLGFLGAGSTMGATSMALTV 566

RESULT 15
 US-10-70-507-121
 Sequence 121, Application US/10780507
 Publication No. US20050137387A1
 GENERAL INFORMATION:
 APPLICANT: MULLINS, James I.
 APPLICANT: RODRIGO, Allen G.
 APPLICANT: LEARN, Gerald H.
 APPLICANT: LI, Fusheng
 APPLICANT: NICKLE, David C.
 APPLICANT: JENSEN, Mark A.
 TITLE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPOUNDS
 FILE REFERENCE: 16336-001320US
 CURRENT APPLICATION NUMBER: US/10/780,507
 CURRENT FILING DATE: 2004-02-17
 PRIOR APPLICATION NUMBER: US 10/204,204
 PRIOR FILING DATE: 2001-02-16
 PRIOR APPLICATION NUMBER: PCT/US01/05288
 PRIOR FILING DATE: 2001-02-16
 PRIOR APPLICATION NUMBER: US 60/183,659
 PRIOR FILING DATE: 2000-02-18
 PRIOR APPLICATION NUMBER: US 60/447,586
 PRIOR FILING DATE: 2003-02-14
 NUMBER OF SEQ ID NOS: 125
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 121
 LENGTH: 883
 TYPE: PRT
 FEATURE:
 OTHER INFORMATION: Deduced ancestor env protein sequence

US-10-780-507-121

Query Match 93.5%; Score 130; DB 5; Length 883;
 Best Local Similarity 93.1%; Pred. No. 1.4e-08;
 Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVGMIGAMFLGFLGAGSTMGATSMALTV 29
 Db 538 AVGMIGAMFLGFLGAGSTMGATSMALTV 566

Search completed: March 7, 2006, 17:56:39
 Job time : 10.4528 secs

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OM protein - protein search, using sw model

Run on: March 7, 2006, 17:53:05 ; Search time 1.11209 Seconds
 (without alignments)
 521.549 Million cell updates/sec

Title: US-09-938-406-1_COPY_523_551

Perfect score: 139

Sequence: 1 AVMLGAMFLGFLGAAAGSTMGATSMALTV 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 135346 seqs, 20000420 residues

Total number of hits satisfying chosen parameters: 135346

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_New:
 1: /cgn2_6/pidata/1/pubpaas/US08_NEW_PUB_pep:
 2: /cgn2_6/pidata/1/pubpaas/US06_NEW_PUB_pep:
 3: /cgn2_6/pidata/1/pubpaas/US07_NEW_PUB_pep:
 4: /cgn2_6/pidata/1/pubpaas/PCT_NEW_PUB_pep:
 5: /cgn2_6/pidata/1/pubpaas/US05_NEW_PUB_pep:
 6: /cgn2_6/pidata/1/pubpaas/US10_NEW_PUB_pep:
 7: /cgn2_6/pidata/1/pubpaas/US11_NEW_PUB_pep:
 8: /cgn2_6/pidata/1/pubpaas/US60_NEW_PUB_pep:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1		109.5	78.8	856	6 US-10-510-947-8	Sequence 8, Appl
2		109.5	78.8	856	7 US-11-042-988-13	Sequence 13, Appl
3		109.5	78.8	856	7 US-11-135-235-1	Sequence 1, Appl
4		104.5	75.2	601	7 US-11-014-842A-37	Sequence 37, Appl
5		104.5	75.2	613	7 US-11-014-842A-33	Sequence 33, Appl
6		104.5	75.2	669	7 US-11-014-842A-29	Sequence 29, Appl
7		104.5	75.2	681	7 US-11-014-842A-25	Sequence 25, Appl
8		104.5	75.2	789	7 US-11-014-842A-39	Sequence 39, Appl
9		104.5	75.2	801	7 US-11-014-842A-35	Sequence 35, Appl
10		104.5	75.2	854	7 US-11-022-562-219	Sequence 219, Appl
11		104.5	75.2	857	7 US-11-014-842A-31	Sequence 31, Appl
12		104.5	75.2	869	7 US-11-014-842A-27	Sequence 27, Appl
13		99.5	71.6	35	7 US-11-096-725-35	Sequence 35, Appl
14		84	60.4	28	7 US-11-223-599A-96	Sequence 96, Appl
15		84	60.4	28	7 US-11-121-566A-96	Sequence 96, Appl
16		84	60.4	30	6 US-10-923-112A-30	Sequence 30, Appl
17		79	56.8	21	7 US-11-078-256-288	Sequence 288, Appl
18		79	56.8	27	6 US-10-985-126-3	Sequence 3, Appl
19		79	56.8	27	7 US-11-067-092A-11	Sequence 29, Appl
20		79	56.8	27	7 US-11-016-542-5	Sequence 5, Appl
21		77	55.4	17	6 US-10-023-112A-29	Sequence 29, Appl
22		77	55.4	17	7 US-11-223-599A-7	Sequence 7, Appl
23		77	55.4	17	7 US-11-121-566A-7	Sequence 7, Appl
24		74	53.2	15	7 US-11-045-024-1977	Sequence 12987, A
25		73.5	52.9	28	7 US-11-141-725-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
 US-10-510-947-8
 Sequence 8, Application US10510947
 ; Publication No. US20050255123A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Trustees of the University of Pennsylvania
 ; APPLICANT: Wilson, James M.
 ; APPLICANT: Medina, Maria Fe C.
 ; APPLICANT: Kobinger, Gary
 ; TITLE OF INVENTION: Chimeric Ebola Virus Envelopes and Uses Therefor
 ; FILE REFERENCE: UPN-02811ECT
 ; CURRENT APPLICATION NUMBER: US10/510,947
 ; CURRENT FILING DATE: 2004-10-28
 ; PRIOR APPLICATION NUMBER: US 60/376,480
 ; PRIOR FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/385,704
 ; PRIOR FILING DATE: 2002-06-04
 ; PRIOR APPLICATION NUMBER: US 60/427,752
 ; PRIOR FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 8
 ; LENGTH: 856
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus type 1
 US-10-510-947-8

Query Match 78.8%; Score 109.5; DB 6; Length 856;
 Best Local Similarity 82.8%; Pred. No. 5.2e-07;
 Matches 24; Conservative 2; Mismatches 2;
 Indels 1; Gaps 1;

Qy 1 AVGGMGAMFIGFLGAGSTMGATSMALTV 29
 Db 512 AVG-1GALFIGFLGAGSTMGATSMALTV 539

RESULT 2
 US-11-042-988-13
 Sequence 13, Application US/11042988
 ; Publication No. US20050244818A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SILICIANO, ROBERT
 ; APPLICANT: ZHANG, HAILI
 ; APPLICANT: ZHOU, YAN
 ; TITLE OF INVENTION: SINGLE CELL ANALYSIS OF HIV REPLICATION CAPACITY AND DRUG RESISTANCE
 ; FILE REFERENCE: 62760 (7159)
 ; CURRENT APPLICATION NUMBER: US/11/042,988

CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/540,716
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO: 13
; LENGTH: 856
; ORGANISM: Human immunodeficiency virus type 1
; JS-11-042-988-13

Query Match Score 78.8%; Best Local Similarity 92.8%; Pred. No. 5.2e-07; Length 856; Matches 24; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

RESULT 3
US-11-135-235-1
; Sequence 1, Application US/11135235
; Publication No. US20060019395A1
; GENERAL INFORMATION:
; APPLICANT: Marasco, Wayne
; TITLE OF INVENTION: Lentiviral Vectors and Uses Thereof
; TITLE REFERENCE: 20163-07
; CURRENT APPLICATION NUMBER: US/11/135,235
; CURRENT FILING DATE: 2005-05-23
; PRIORITY NUMBER: 60/589,610
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 1
; LENGTH: 856
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; JS-11-135-235-1

Query Match Score 78.8%; Best Local Similarity 92.8%; Pred. No. 5.2e-07; Length 856; Matches 24; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

RESULT 4
US-11-014-842A-37
Sequence 37, Application US/11014842A
Publication No. US20060013826A1
; GENERAL INFORMATION:
; APPLICANT: TANGI, FREDERIC
; APPLICANT: LORIN, CLARISSÉ
; APPLICANT: DELEBECQUE, FREDERIC
; APPLICANT: MOLLET, LUCILE
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPE OF ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF VACCINE COMPOSITIONS
; CURRENT APPLICATION NUMBER: US/11/014,842A
; CURRENT FILING DATE: 2004-12-20
; PRIORITY NUMBER: PCT/EP03/07146
; PRIOR APPLICATION NUMBER: EP 02291550.8
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO: 3
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; JS-11-014-842A-37

Query Match Score 75.2%; Best Local Similarity 79.3%; Pred. No. 1.6e-06; Length 601; Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

RESULT 5
US-11-014-842A-33
; Sequence 33, Application US/11014842A
; Publication No. US20060013826A1
; GENERAL INFORMATION:
; APPLICANT: TANGI, FREDERIC
; APPLICANT: LORIN, CLARISSÉ
; APPLICANT: MOLLET, LUCILE
; APPLICANT: DELEBECQUE, FREDERIC
; APPLICANT: MOLLET, LUCILE
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPE OF ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF VACCINE COMPOSITIONS
; FILE REFERENCE: 2356..0093
; CURRENT APPLICATION NUMBER: US/11/014,842A
; CURRENT FILING DATE: 2004-12-20
; PRIORITY NUMBER: PCT/EP03/07146
; PRIOR APPLICATION NUMBER: EP 02291550.8
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO: 29
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; JS-11-014-842A-33

Query Match Score 104.5%; Best Local Similarity 79.3%; Pred. No. 1.6e-06; Length 613; Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

RESULT 6
US-11-014-842A-29
; Sequence 29, Application US/11014842A
; Publication No. US20060013826A1
; GENERAL INFORMATION:
; APPLICANT: TANGI, FREDERIC
; APPLICANT: LORIN, CLARISSÉ
; APPLICANT: DELEBECQUE, FREDERIC
; APPLICANT: MOLLET, LUCILE
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPE OF ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF VACCINE COMPOSITIONS
; FILE REFERENCE: 2356..0093
; CURRENT APPLICATION NUMBER: US/11/014,842A
; CURRENT FILING DATE: 2004-12-20
; PRIORITY NUMBER: PCT/EP03/07146
; PRIOR APPLICATION NUMBER: EP 02291550.8
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO: 29
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; JS-11-014-842A-29

US-11-014-842A-29

Query Match 75.2%; Score 104.5; DB 7; Length 69;
Best Local Similarity 79.3%; Pred. No. 1.8e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy 1 AVGMLGAMPLGFLGAGSTMGATSMALTY 29
Db 498 AVG-IGAVFLGFLGAGSTMGAASTLV 525

RESULT 7

US-11-014-842A-25

; Sequence 25, Application US/11014842A
; Publication No. US20060013826A1
; GENERAL INFORMATION:
; APPLICANT: TANGY, FREDERIC
; APPLICANT: LORIN, CLARISSE
; APPLICANT: MOLLET, LUCILE
; APPLICANT: DELBECQUE, FREDERIC
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPE OF
; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
; TITLE OF INVENTION: VACCINE COMPOSITIONS
; FILE REFERENCE: 2356_0093
; CURRENT APPLICATION NUMBER: US/11/014, 842A
; CURRENT FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: PCT/EP03/07146
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02291550.8
; PRIOR FILING DATE: 2002-06-20
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO: 25
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-014-842A-25

Query Match 75.2%; Score 104.5; DB 7; Length 681;
Best Local Similarity 79.3%; Pred. No. 1.8e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy 1 AVGMLGAMPLGFLGAGSTMGATSMALTY 29
Db 510 AVG-IGAVFLGFLGAGSTMGAASTLV 537

RESULT 8

US-11-014-842A-39

; Sequence 39, Application US/11014842A
; Publication No. US20060013826A1
; GENERAL INFORMATION:
; APPLICANT: TANGY, FREDERIC
; APPLICANT: LORIN, CLARISSE
; APPLICANT: MOLLET, LUCILE
; APPLICANT: DELBECQUE, FREDERIC
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPE OF
; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
; TITLE OF INVENTION: VACCINE COMPOSITIONS
; FILE REFERENCE: 2356_0093
; CURRENT APPLICATION NUMBER: US/11/014, 842A
; CURRENT FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: PCT/EP03/07146
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02291550.8
; PRIOR FILING DATE: 2002-06-20
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO: 39
; LENGTH: 789
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-014-842A-39

Query Match 75.2%; Score 104.5; DB 7; Length 789;
Best Local Similarity 79.3%; Pred. No. 2.2e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy 1 AVGMLGAMPLGFLGAGSTMGATSMALTY 29
Db 430 AVG-IGAVFLGFLGAGSTMGAASTLV 457

RESULT 9

US-11-014-842A-35

; Sequence 35, Application US/11014842A
; Publication No. US20060013826A1
; GENERAL INFORMATION:
; APPLICANT: TANGY, FREDERIC
; APPLICANT: LORIN, CLARISSE
; APPLICANT: MOLLET, LUCILE
; APPLICANT: DELBECQUE, FREDERIC
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPE OF
; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
; TITLE OF INVENTION: VACCINE COMPOSITIONS
; FILE REFERENCE: 2356_0093
; CURRENT APPLICATION NUMBER: US/11/014, 842A
; CURRENT FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: PCT/EP03/07146
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02291550.8
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO: 35
; LENGTH: 801
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-014-842A-35

Query Match 75.2%; Score 104.5; DB 7; Length 801;
Best Local Similarity 79.3%; Pred. No. 2.2e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy 1 AVGMLGAMPLGFLGAGSTMGATSMALTY 29
Db 442 AVG-IGAVFLGFLGAGSTMGAASTLV 469

RESULT 10

US-11-022-562-219

; Sequence 219, Application US/11022562
; Publication No. US2005024942A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022, 562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSEQ For Windows Version 4.0
; SEQ ID NO: 219
; LENGTH: 854
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-11-022-562-219

Query Match 75.2%; Score 104.5; DB 7; Length 854;
Best Local Similarity 79.3%; Pred. No. 2.4e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy 1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29
 Db 510 AVG-IGAVFLGFLGAAGSTMGAASVTLY 537

RESULT 11
 US-11-014-842A-31
 ; Sequence 31; Application US/11014842A
 ; Publication No. US20060013826A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TANGY, FREDERIC
 ; APPLICANT: LORIN, CLARISSE
 ; APPLICANT: MOLLET, LUCILE
 ; APPLICANT: DELEBECQUE, FREDERIC
 ; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPE OF
 ; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
 ; TITLE OF INVENTION: VACCINE COMPOSITIONS
 ; FILE REFERENCE: 2356 0093
 ; CURRENT APPLICATION NUMBER: US/11/014, 842A
 ; CURRENT FILING DATE: 2004-12-20
 ; PRIORITY APPLICATION NUMBER: PCT/EP03/07146
 ; PRIOR FILING DATE: 2003-06-20
 ; PRIORITY APPLICATION NUMBER: EP 02291550 .8
 ; PRIOR FILING DATE: 2002-06-20
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn Ver. 3.3
 ; SEQ ID NO 31
 ; LENGTH: 657
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus type 1
 US-11-014-842A-31

Query Match 75.2%; Score 104.5; DB 7; Length 857;
 Best Local Similarity 79.3%; Pred. No. 2.4e-06;
 Matches 23; Conservative 3; Mismatches 2;
 Indels 1; Gaps 1;

Qy 1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29
 Db 498 AVG-IGAVFLGFLGAAGSTMGAASVTLY 525

RESULT 12
 US-11-014-842A-27
 ; Sequence 27; Application US/11014842A
 ; Publication No. US20060013826A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TANGY, FREDERIC
 ; APPLICANT: LORIN, CLARISSE
 ; APPLICANT: MOLLET, LUCILE
 ; APPLICANT: DELEBECQUE, FREDERIC
 ; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPE OF
 ; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
 ; TITLE OF INVENTION: VACCINE COMPOSITIONS
 ; FILE REFERENCE: 2356 0093
 ; CURRENT APPLICATION NUMBER: US/11/014, 842A
 ; CURRENT FILING DATE: 2004-12-20
 ; PRIORITY APPLICATION NUMBER: PCT/EP03/07146
 ; PRIOR FILING DATE: 2003-06-20
 ; PRIORITY APPLICATION NUMBER: EP 02291550 .8
 ; PRIOR FILING DATE: 2002-06-20
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn Ver. 3.3
 ; SEQ ID NO 27
 ; LENGTH: 869
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus type 1
 US-11-014-842A-27

Query Match 75.2%; Score 104.5; DB 7; Length 869;
 Best Local Similarity 79.3%; Pred. No. 2.4e-06;
 Matches 23; Conservative 3; Mismatches 2;
 Indels 1; Gaps 1;

Qy 1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29
 Db 510 AVG-IGAVFLGFLGAAGSTMGAASVTLY 537

RESULT 13
 US-11-056-725-35
 ; Sequence 35; Application US/11096725
 ; Publication No. US20060013820A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BONNET, Dominique
 ; APPLICANT: BROWN, Carleton B
 ; APPLICANT: GEORGES, Bertrand
 ; APPLICANT: SIZER, Philip J
 ; TITLE OF INVENTION: Antigen Delivery Vectors and Constructs
 ; FILE REFERENCE: KLB-001
 ; CURRENT APPLICATION NUMBER: US/11/096, 725
 ; CURRENT FILING DATE: 2005-04-01
 ; PRIORITY APPLICATION NUMBER: GB0408164 .2
 ; PRIOR FILING DATE: 2004-04-13
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 35
 ; LENGTH: 35
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus type 1
 US-11-096-725-35

Query Match 71.6%; Score 99.5; DB 7; Length 35;
 Best Local Similarity 88.0%; Pred. No. 3.1e-07;
 Matches 22; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 AVGMLGAMFLGFLGAAGSTMGATSM 25
 Db 11 AVG-IGAMFLGFLGAAGSTMGAASM 34

RESULT 14
 US-11-223-699A-96
 ; Sequence 96; Application US/11223699A
 ; Publication No. US20060035815A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHEN, LISHAN
 ; APPLICANT: CUI, KUNYUAN
 ; APPLICANT: HOUSTON, JR., MICHAEL E.
 ; APPLICANT: MAYER, SASHA
 ; APPLICANT: CHEN, YUCHING
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR DELIVERY OF
 ; TITLE OF INVENTION: RIBONUCLEIC ACID TO A CELL
 ; FILE REFERENCE: 04-03CIP
 ; CURRENT APPLICATION NUMBER: US/11/223, 699A
 ; CURRENT FILING DATE: 2005-19-08
 ; PRIORITY APPLICATION NUMBER: 11/121, 566
 ; PRIORITY FILING DATE: 2005-05-04
 ; PRIORITY APPLICATION NUMBER: 60/667, 833
 ; PRIORITY FILING DATE: 2005-04-01
 ; PRIORITY APPLICATION NUMBER: 60/656, 572
 ; PRIORITY FILING DATE: 2005-02-25
 ; PRIORITY APPLICATION NUMBER: 60/613, 416
 ; PRIORITY FILING DATE: 2004-09-27
 ; PRIORITY APPLICATION NUMBER: 60/570, 513
 ; PRIORITY FILING DATE: 2004-05-12
 ; PRIORITY APPLICATION NUMBER: 60/570, 512
 ; PRIORITY FILING DATE: 2004-05-12
 ; PRIORITY APPLICATION NUMBER: 60/568, 027
 ; NUMBER OF SEQ ID NOS: 175
 ; SOFTWARE: PatentIn Ver. 3.3
 ; SEQ ID NO 96
 ; LENGTH: 28
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide
 US-11-223-699A-96

Query Match 60.4%; Score 84; DB 7; Length 28;
 Best Local Similarity 89.5%; Pred. No. 2.6e-05;
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 6 GAMFGLGAGSTMGAT\$ 24
 Db 1 GALFLGFLAGSTMGAW\$ 19

RESULT 15

US-11-121-566A-96

Sequence 96, Application US/11121566A

Publication No. US20060040882A1

GENERAL INFORMATION:

APPLICANT: CHEN, LISHAN

CUI, KUNYUAN

CHEN, YUCHING

MAYER, SASHA

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING DELIVERY OF

TITLE OF INVENTION: NUCLEIC ACIDS INTO CELLS AND FOR MODIFYING EXPRESSION

TITLE OF INVENTION: TARGET GENES IN CELLS

FILE REFERENCE: 04-01015

CURRENT APPLICATION NUMBER: US/11/121,566A

CURRENT FILING DATE: 2005-05-04

PRIOR APPLICATION NUMBER: 60/667,833

PRIOR FILING DATE: 2005-04-01

PRIOR APPLICATION NUMBER: 60/656,572

PRIOR FILING DATE: 2005-02-25

PRIOR APPLICATION NUMBER: 60/613,416

PRIOR FILING DATE: 2004-09-27

PRIOR APPLICATION NUMBER: 60/570,513

PRIOR FILING DATE: 2004-05-12

PRIOR APPLICATION NUMBER: 60/570,512

PRIOR FILING DATE: 2004-05-12

PRIOR APPLICATION NUMBER: 60/568,027

PRIOR FILING DATE: 2004-05-04

NUMBER OF SEQ ID NOS: 163

SOFTWARE: PatentIn Ver. 3.3

SEQ ID NO: 96

LENGTH: 28

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Peptide

US-11-121-566A-96

Query Match 60.4%; Score 84; DB 7; Length 28;
 Best Local Similarity 89.5%; Pred. No. 2.6e-05;
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GAMFGLGAGSTMGAT\$ 24

Db 1 GALFLGFLAGSTMGAW\$ 19

Search completed: March 7, 2006, 17:57:11
 Job time : 2.11209 secs

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CC or eukaryotic cell transfected with the expression
 CC construct; a composition for inducing an immune response in a mammal
 CC comprising a highly diverse FIV ancestor protein or its antigenic
 CC fragment; a method of preparing an FIV viral amino acid sequence; a
 CC method for inducing an immune response to FIV in a host; a method for
 CC making an FIV vaccine; a kit comprising a composition comprising an FIV
 CC ancestor protein or an antigenic fragment of an FIV ancestor protein and
 CC instructions for administering the composition to a subject; and a method
 CC for detecting infection with FIV. The ancestral feline immunodeficiency
 CC virus (FIV) nucleic acid sequence is useful in preparing a vaccine
 CC against FIV. This is the amino acid sequence of ancestral HIV-1 group M
 CC subtype B envelope (env) protein.
 XX

Sequence 883 AA:

Query Match	85.7%	Score 2977.5;	DB 9;	Length 883;
Best Local Similarity	84.7%	Pred. No. 1.1e-159;		
Matches 564;	Conservative	27;	Mismatches 54;	Indels 21;
				Gaps 6;

Qy 3 LMVTVYGGPVWKEATTLFCASDAKAYDTAAHNTWATHACVPTNPNPQEVLNEYTF 62
 Db 33 LMVTVYGGPVWKEATTLFCASDAKAYDTAAHNTWATHACVPTDNPQEVLNEYTF 92
 Qy 63 NMWKNNMVEQMHEDIIISLWDSLKPCVKLPLCIVTLCNTDLNTNTNTTFLS1IVVWEQ 122
 Db 93 NMWKNNMVEQMHEDIIISLWDSLKPCVKLPLCIVTLCNTDLRTNTNTNTTATTNTS 152
 Qy 123 RG-----KGEMRNSFNITTSIRDVKREYALFVKLDEPID-DNKRTNTNNTKYRLIN 174
 Db 153 SGGGTMEGEGEIKNSFNITTSIRDQMEYALFYKLDDVVPIDDNNTNTNTNTSYRLIN 212
 Qy 175 CNTSVITQACPVSSEPTIPIHTYCTPQFALLKCNDKFNGTGPCTINVSYCTQCTHGRPVV 234
 Db 213 CNTSVITQACPVSSEPTIPIHTYCTPQFALLKCNDKFNGTGPCTINVSYCTQCTHGRPVV 272
 Qy 235 STOLLINGSLAEEEVIRSENFTNNAKTIIVOLNVSVEINCTRPNHTRKRVTLGPGRTW 294
 Db 273 STOLLINGSLAEEEVIRSENFTNNAKTIIVOLNVSVEINCTRPNHTRKRVTLGPGRTW 332
 Qy 295 YTPGEILGNIROAHCNISRAQWNTLQIAITLRLBFGN⁻-TIAFNQSISGDPBTWMS 352
 Db 333 YATGKLGIDIROAHCNLSRAKWNNTLKQIVTKLQRQGNNKTTIVPNQSSGGDPBTWMS 392
 Qy 353 FNCGGBFFYCNISTOLFNSANNTVSNTGNTWSVTTRKOK---DTGDLTITLPCKRICKTINRQ 407
 Db 393 FNCGGBFFYCNISTOLFNSANNTVSNTGNTWSVTTRKOK---DTGDLTITLPCKRICKTINRQ 450
 Qy 408 VIGKAMYALPKLGLRCNSNTGLLTRDGGENOT---TEIIPRGCGDMRDWRSELY 463
 Db 451 EVGKAMYAPPSQGLRCNSNTGLLTRDGGENNTNTDTEIIPRGCGDMRDWRSELY 510
 Qy 464 KYKVKIEPLGAVAPTKARRVQREGAVMLGAMFLGFQGAAGTMGATSMALTVQARQ 523
 Db 511 KYKVKIEPLGAVAPTKARRVQREGAVMLGAMFLGFQGAAGTMGATSMALTVQARQ 570
 Qy 524 LLSGIVYQQNLLRAKAQHLLQDLYTGWLKQLQARLAVERYLKDQQLIGFWGCSGKUJ 583
 Db 571 LLISGIVYQQNLLRAEAQHLLQDLYTGWLKQLQARLAVERYLKDQQLIGFWGCSGKUJ 630
 Qy 584 CTTAVPNWNSKNSKLDQIWNNTMNEWDREIDNTHTLITLIESQNQEBKNOELQJL 643
 Db 631 CTTAVPNWNSKNSKLDQIWNNTMNEWDREIDNTGLVYLIESQNQEBKNOELQJL 690
 Qy 644 DKWASL 649
 Db 691 DKWASL 696

XX	19-MAY-2005	(first entry)
XX	DT	
XX	DE	
XX	Xenotransplantation; vaccine; acquired immune deficiency syndrome; anti-hiv; immune disorder; HIV-1 infection; infection; PERV infection; diagnosis; graft versus host disease; immunosuppressive; envelope protein.	
XX	KW	
OS	Human immunodeficiency virus 1; subtype B.	
OS	Synthetic.	
XX	OS	
XX	PN	WO2005019411-A2.
XX	XX	
PD	03-MAR-2005.	
XX	PP	2004W0-US015709.
XX	PR	2003US-0041949.
XX	PA	(AUCK-) AUCKLAND UNISERVICES LTD. (UNIW) UNIV WASHINGTON.
XX	PI	Mullins JI, Rodrigo A, Ross HA;
XX	DR	WPI; 2005-2025/21. N-PDB; ADY27997.
XX	DR	New isolated ancestral viral nucleic acid sequence that is a determined founder sequence of a highly diverse viral strain, subtype or group of an endogenous retrovirus, useful in the prophylaxis of viral infection.
XX	PT	New isolated ancestral viral nucleic acid sequence that is a determined founder sequence of a highly diverse viral strain, subtype or group of an endogenous retrovirus, useful in the prophylaxis of viral infection.
XX	PT	Disclosure; SEQ ID NO 2; 271pp; English.
XX	CC	The invention relates to an isolated ancestral viral nucleic acid sequence and its fragment, where the sequence is a determined founder sequence of a highly diverse viral strain, subtype or group of an endogenous retrovirus. Also included are an isolated ancestor protein (or its fragment) from an endogenous retrovirus, an isolated expression construct (comprising the following operably linked elements: a transcriptional promoter; a nucleic acid encoding an endogenous retrovirus ancestor protein and a transcriptional terminator), a cultured prokaryotic (or eukaryotic cell) transformed or transfected with the expression construct, an isolated host cell comprising the expression construct, a composition for inducing an immune response in a recipient mammal (comprising a viral ancestor protein or its antigenic fragment, where the protein is from a virus of a donor species); an isolated antibody that binds specifically to an endogenous retrovirus ancestor protein (and that binds specifically to a plurality of circulating descendant endogenous retrovirus ancestor proteins), a method of preparing an ancestral endogenous retroviral amino acid sequence, a method for inducing an immune response to a donor virus in a transplant recipient or a potential transplant recipient, a method of making a vaccine, a method for detecting infection with an endogenous retrovirus and a method for performing xenotransplantation in a subject. The ancestral viral nucleic acid sequence is of Porcine Endogenous Retrovirus (PERV) subtype A, B or C and has at least 70% identity with sequence of any of the 18 nucleotide sequences fully defined in the specification. The sequence may also be optimized for expression in a human host. The nucleic acid sequence or its fragment is useful in the prophylaxis of viral infection in transplantation that is heightened by the presence of factors commonly associated with viral activation, e.g. immune suppression, graft versus host disease, graft rejection, viral co-infection, and cytotoxic therapies. The present sequence is an ancestral HIV-1 env protein.
SQ	Sequence 883 AA;	

Query Match 85.7%; Score 2977.5; DB 9; Length 883;
 Best Local Similarity 84.7%; Pred. No. 1.1e-159;
 Matches 564; Conservative 27; Mismatches 54; Indels 21; Gaps 6;

RESULT 6
 ADY27998
 ID ADY27998 standard; protein: 883 AA.
 XX ADY27998

PR	14-FEB-2003 ; 2003US-0447586P.
QY	3 LWTIVYYGPPWKEATTTLFCASDAKAYTEAIIINWATHACVPTNPQEVLVENTF 62 33 LWTIVYYGPPWKEATTTLFCASDAKAYTEAIIINWATHACVPTDNPQEVLVENTF 92
Db	63 NMWKNMVMQMHEDTISLMDQSLSRCPVKLTPCLVNLCDLRTNANTINSSATNTTS 122 93 NMWKNMVMQMHEDTISLMDQSLSRCPVKLTPCLVNLCDLRTNANTINSSATNTTS 152
QY	123 RG-----KGEMLNCSEWTTTSIRDKYOREALFYKLDEPEID-DNKNTTNTKYRLIN 174 153 SGGTMEGEGEIKNCSEWTTTSIRDKYOREALFYKLDEPEIDDNNNNTNTSYRLIN 212
Db	175 CNTSVITQCPKVSFPIIHYCPTGPALKNDKENGTPCTNVSTQCTHGRPVV 234 213 CNTSVITQCPKVSFPIIHYCPTGPALKNDKENGTPCTNVSTQCTHGRPVV 272
QY	235 STQLLNGSLAEEEVVIRESENFTNAKTLIVQLNVSVEINCTRNHHTRKRVTLGPRGVW 294 273 STQLLNGSLAEEEVVIRESENFTNAKTIIVQLNVSVEINCTRNHHTRKRVTLGPRGVW 332
Db	295 YTGBEILGNIROAHNCNSRAQWNTLQIAATTLEQFGNK-TIAFNQSGGDPPEIVMHS 352 333 YATSKIGIIGTROAHNCNSRAKWNNTLKQIVTKLREQFGNKTTIVENQSGGDPPEIVMHS 392
QY	353 FNGCGEFFTCNSTOLPNSWNTSNGTWSVTROK---DTGDIITLPCRKIQIINNWQ 407 393 FNGCGEFFTCNSTOLPNSWHF--NGTWGNNNTERSNNADDNTITLEPCRKIQIINNWQ 450
Db	408 VVGRAMYALPIKGHLRCSSNITGLLTRDGGENOT---TEFRPGCCGDMRNUWRSEL 463 451 EVGKAMYAPPISQJRCSSNITGLLTRDGGENOT---TEFRPGCCGDMRNUWRSEL 510
QY	464 KYKVVKIEPLGVAPTTKAERVYQREKAVGMGLAMPGLIGAAGSTMCAATSMALTQARQ 523 511 KYKVVKIEPLGVAPTTKAERVYQREKAVGMGLAMPGLIGAAGSTMGAASMLTVQARQ 570
Db	524 LLGGIVQQNNLRAIKAQHQLQLTWIKOQARILLAVERTLKDQOLGFWMGCSGKLI 583 571 LLGGIVQQNNLRAIKAQHQLQLTWIKOQARILLAVERTLKDQOLGFWMGCSGKLI 630
QY	584 CTTAVPWNASWSNKTLDQIWNNTMWTMENDTIDNYTHLTYLTTEESONQKBNOQEYLQI 643 631 CTTAVPWNASWSNKTLDQIWNNTMWTMENDTIDNYTGILTYLTTEESONQKBNOQEYLQI 690
Db	644 DKWASL 649 631 DKWASL 696
QY	REFRESULT 7 AEE10654 standard; protein; 883 AA. AEE10654;
Db	25-AUG-2005 (first entry) AN1-Env ancestor protein, SEQ ID NO: 121.
QY	Immune stimulation; diagnosis; gene therapy; viral infection; viricide; infection; HIV infection; anti-hiv; ancestor protein. Synthetic.
Db	US2005137387-A1. 23-JUN-2005.
QY	511 KYKVVKIEPLGVAPTTKAERVYQREKAVGMGLAMPGLIGAAGSTMGAASMLTVQARQ 570
Db	524 LLGGIVQQNNLRAIKAQHQLQLTWIKOQARILLAVERTLKDQOLGFWMGCSGKLI 583 571 LLGGIVQQNNLRAIKAQHQLQLTWIKOQARILLAVERTLKDQOLGFWMGCSGKLI 630
QY	584 CTTAVPWNASWSNKTLDQIWNNTMWTMENDTIDNYTGILTYLTTEESONQKBNOQEYLQI 690

XX	WPI: 2005-242571/25. DR N-PSDB; AD207747.	QY 543 QHLJLQTWIKOLQARILAVERYIKDQQLGFWNGCSGKLICTTAPVNNAWSNKTLDDQI 602 557 QHLJLQTWIKOLQARILAVERYIKDQQLGFWGSGRKLICITPWNNAWSNKSLDEI 616
XX	New isolated consensus or ancestral immunogenic proteins, useful for inducing antibodies that neutralize a wide spectrum of human immunodeficiency virus (HIV) primary isolates and/or that induces a T cell response.	Db 603 WANNTMWENDREIDNYTHLILYTIESONQEBKNQQELIQLDKWASL 649 617 WDNNTMWEWEREIDNYTSLIYTIESONQERNEQELIQLDKWASL 663
PS	Example 7; Fig 20D; 284pp; English.	RESULT 10 AEB10583 ID AEB10583 standard; protein; 862 AA. XX AC AEB10583; XX DT 25-AUG-2005 (first entry) XX DE Clade B env (gp160) protein, Bgp160.mrca, SEQ ID NO: 50. XX DE Immune stimulation; diagnosis; gene therapy; viral infection; virucide; KW infection; HIV infection; anti-hiv; env protein. XX OS Synthetic. XX PN US2005137387-A1. XX PD 23-JUN-2005. XX PR 18-FEB-2000; 2000US-0183659P. XX PR 17-FEB-2004; 2004US-00780507. XX PR 18-FEB-2000; 2000US-0183659P. PR 16-FEB-2001; 2001WO-US005288. PR 14-FEB-2003; 2003US-0447866. DR N-PSDB; AEB10560.
XX	The invention describes an isolated protein (I) selected from 106 fully defined 500-866 amino acid sequences given in the specification. Also described are: a nucleic acid comprising: a nucleotide sequence encoding CON6 HIV gp160 protein, subtype C ancestral HIV envelope protein, subtype C consensus HIV envelope protein, subtype C consensus HIV gag protein, subtype C consensus HIV nef protein, Group M consensus HIV envelope protein, subtype A consensus HIV envelope protein, Group M consensus HIV gag protein, Group M consensus HIV pol protein, Group M consensus HIV nef protein, subtype C consensus HIV pol protein, subtype B consensus HIV gag protein, or subtype B consensus HIV envelope protein, where the nucleotide sequence comprises codons optimized for expression in human cells; a nucleotide sequence encoding (I); or a nucleotide sequence selected from 89 fully defined 633-2607 bp sequences given in the specification; a vector comprising the nucleic acid of (I); a composition comprising at least one protein or nucleic acid above and a carrier; and inducing an immune response in a mammal. The protein is a consensus or ancestral immunogen useful for inducing antibodies that neutralize a wide spectrum of HIV primary isolates and/or that induces a T cell response. This is the amino acid sequence of HIV subtype B consensus env protein. Sequence 850 AA;	PA (UNIW) UNIV WASHINGTON OFFICE TECHNOLOGY TRANSF. PI Mullins JI, Rodrigo AG, Learn GH, Li F, Nickle DC, Jensen MA, XX DR WPI, 2005-441181/45. XX PT New isolated ancestral or COT viral nucleic acid and amino acid sequences that are determined founder sequences of a highly diverse viral strain, PT useful for diagnosing, preventing or treating viral (e.g. HIV) infection. PT PR 16-FEB-2001; 2001WO-US005288. PR 14-FEB-2003; 2003US-0447866. DR N-PSDB; AEB10560. XX PT Claim 11; SEQ ID NO 50; 201pp; English. XX PS The invention relates to an ancestral or center of tree (COT) viral nucleic acid and amino acid sequences that are determined founder sequences of a highly diverse viral strain. The invention also relates to a composition comprising a highly diverse viral ancestor protein or an immunogenic fragment of an ancestor or COT protein for inducing an immune response in a mammal and a method for preparing an ancestral or COT viral amino acid sequence. The composition and methods are useful for diagnosing, preventing or treating viral (e.g. HIV) infection. The invention is also useful in gene therapy. The present sequence is a clade B env (gp160) protein. This sequence is used in the comparison of the most recent common ancestor (MRCA), COT least squares (LScot) and COT minimum of means (MMcot) reconstructions for the clade B env gene. Sequence 862 AA;
QY	3 LWVTTYYGPVWKEATTIILCASDAKAYDEARNWATACVPTNPNVBEVLENVENTF 62 63 NMWQRNRMVEQNMHDITSLMDQSLLKEPCVKLPLCVTLNCTDLNNTNTTELSIIVWWQ 122 93 NMWQRNRMVEQNMHDITSLMDQSLLKEPCVKLPLCVTLNCTDLK-NMLNTNSSS---GEK 147	Query Match Score 2970; DB 9; Length 850; Best Local Similarity 86.9%; Pred. No. 2.8e-159; Matches 562; Conservative 30; Mismatches 39; Indels 16; Gaps 7;
Db	33 LWVTTYYGPVWKEATTIILCASDAKAYDEARNWATACVPTNPNVBEVLENVENTF 92	QY 3 LWVTTYYGPVWKEATTIILCASDAKAYDEARNWATACVPTNPNVBEVLENVENTF 62 Db 33 LWVTTYYGPVWKEATTIILCASDAKAYDEARNWATACVPTNPNVBEVLENVENTF 92
QY	123 RGKGEMRNCSFNITISIRDKVQRETAFLYKLDVEPIDDNKNTNTKYLNLNTNTSVIQ 182 148 MEKGPIKNCNSFNITISIRDKVQRETAFLYKLDVPIDNN---NNNTSYRLSNTNSVTIQ 203	Db 33 LWVTTYYGPVWKEATTIILCASDAKAYDEARNWATACVPTNPNVBEVLENVENTF 92
Db	183 ACPKVSFEPIPPIHYCPTPGLFALLKNDKEFKNGTPCINTNSTVQOCTHGRPVSTOLLNG 242 204 ACPKVSFEPIPPIHYCAGAFAILCKNDKEFKNGTPCINTNSTVQOCTHGRPVSTOLLNG 263	QY 123 RGKGEMRNCSFNITISIRDKVQRETAFLYKLDVEPIDDNKNTNTKYLNLNTNTSVIQ 182 Db 148 MEKGPIKNCNSFNITISIRDKVQRETAFLYKLDVPIDNN---NNNTSYRLSNTNSVTIQ 203
QY	243 SLAEEBVRVSENFNTNAKTTIVOLNVSBEINCRTRNNHTRKRVTLGRPVWYTGETIG 302 264 SLAEEBVRVSENFNTDNAKTTIVOLNESTBEINCRTRNNTRKSIIHGPRAPFTGETIG 323	Db 183 ACPKVSFEPIPPIHYCPTPGLFALLKNDKEFKNGTPCINTNSTVQOCTHGRPVSTOLLNG 242 Db 204 ACPKVSFEPIPPIHYCAGAFAILCKNDKEFKNGTPCINTNSTVQOCTHGRPVSTOLLNG 263
QY	303 NIROAHCNNSRAQWNTLQOIAUTLREQGNKNTIAFNQSGGDPEVNHESNGGEEFYC 362 324 DIROAHCNNSRAQWNTLQOIAUTLREQGNKNTIAFNQSGGDPEVNHESNGGEEFYC 383	QY 243 SLAEEBVRVSENFNTNAKTTIVOLNVSBEINCRTRNNHTRKRVTLGRPVWYTGETIG 302 Db 264 SLAEEBVRVSENFNTDNAKTTIVOLNESTBEINCRTRNNTRKSIIHGPRAPFTGETIG 323
QY	363 NSTQLFNSAWNVTNSGTWSVTRKOKDTGDLITLPCRQIINRQVVGKAMYALPIKGII 422 384 NTQLFENSTW - DNGTWN - KDKNT --- ITLPCRQI INNQWEGKAMYAPPIRQI 437	Db 303 NIROAHCNNSRAQWNTLQOIAUTLREQGNKNTIAFNQSGGDPEVNHESNGGEEFYC 362 Db 324 DIROAHCNNSRAQWNTLQOIAUTLREQGNKNTIAFNQSGGDPEVNHESNGGEEFYC 383
Db	422 RCSSNITGILITRDGGGENOTTEIFRGGGDMDRNWRSSLYKVKVLEPLGVAPTKR 482 438 RCSSNITGILITRDGGNNNDTEIFRGGGDMDRNWRSSLYKVKVLEPLGVAPTKR 497	QY 363 NSTQLFNSAWNVTNSGTWSVTRKOKDTGDLITLPCRQIINRQVVGKAMYALPIKGII 422 Db 384 NTQLFENSTW - DNGTWN - KDKNT --- ITLPCRQI INNQWEGKAMYAPPIRQI 437
QY	498 RVVOREKRAVGMGLGFLGAAGSTMCAATSMLTVYQARQLSGIVQQNNLIRATAQ 542 500 RVVOREKRAVG-IGAMFLGFLGAAGSTMCASTSMLTVYQARQLSGIVQQNNLIRATAQ 556	Db 422 RCSSNITGILITRDGGGENOTTEIFRGGGDMDRNWRSSLYKVKVLEPLGVAPTKR 482 Db 438 RCSSNITGILITRDGGNNNDTEIFRGGGDMDRNWRSSLYKVKVLEPLGVAPTKR 497
QY	62 FNNMKNNMVEQMHEDITSLWDQSLKPVCYKLTPLCVTLNCTDINTNTNTTELTSIIVVWE 121	QY 498 RVVOREKRAVG-IGAMFLGFLGAAGSTMCASTSMLTVYQARQLSGIVQQNNLIRATAQ 556

Db 92 ENMKWNMVEQMHDITLWQSLKPCVKLTPLCYTLNCTDAN-KNATNTNSSS---GG 146
 Qy 122 QRGKGMENRNCSEPNITTSIRDVKVQEVALFYKLDVBPIDDNKNTNTKYLINCNTSVIT 181
 Db 147 TMEKGEMKNCSEPNITTSIRDVKVQEVALFYKLDVBPIDDNKNTNTKYLINCNTSVIT 206
 Qy 182 QACPVSFEPPIHYCTPGLFAILKNDKKGENTGPCTINYSTVQCHGIRPVSTOLLIN 241
 Db 207 QACPVSFEPPIHYCTPAGFAILKNDKKGENTGPCKNISTVQCHGIRPVSTOLLIN 266
 Qy 242 GSAEEEVIRSENFTNAKTTIVOLNVNSVBNCTRPNNHTRKRYTLLGPGRVWYTGEIL 301
 Db 267 GSAEEEVIRSENFTNAKTTIVOLNVNSVBNCTRPNNTRKS1PIGGRALYTGEIL 326
 Qy 302 GNIROAHNCISRAQWNTLQLQIAATTREQFG-NKTAIPNQSGGDPBIVNHSFNCGEPP 360
 Db 327 GDIROAHNCISRAKWNNTLKVQVTKUREQFENKNTIVPNPSSGGDPBIVNHSFNCGEPP 386
 Qy 361 YCNSTOLFNSAWNNTENGTSWSVTRKDKTDLITLPCR1KOLINRNQVVGKAMYAAPPNG 420
 Db 387 YCNSTOLFNSAWNNT-EGSNKTTGSNTNGGETITLPCR1KOLINRNQVVGKAMYAAPPNG 445
 Qy 421 LIRCSSNTGILTRDGGENOT-TEIFRPGGDMRDNNRSELTYKVKYKIEPLGVAPT 478
 Db 446 QIKCSSNTGILTRD-GENSTNETFEIPEGGDMRDNNRSELTYKVKYKIEPLGVAPT 504
 Qy 479 KAKRKYVQEKRKAVGMLGAMFLGIGASSTGATSMALTYQARQLLSGYQQQNLLRA 538
 Db 505 KAKRKYVQEKRKAVGMLGAMFLGIGASSTGMAASMTLYQARQLSGIYQQQNLLRA 564
 Qy 539 IKAQHJLLQLTWGKIQLQARTLAYERLYLKDQOLLGFWGCSKLICITTAVWNASWSNKT 598
 Db 565 TEAQHJLLQLTWGKIQLQARTLAYERLYLKDQOLLGFWGCSKLICITTAVWNASWSNKT 624
 Qy 599 LDQIWNMNTWWMDREIDNTHLYTLLIEESONQEQNQELLDKWAHL 649
 Db 625 LDKWNMNTWWMDREIDNTHLYTLLIEESONQEQNQELLDKWAHL 675

RESULT 11
 ADY99903 DT 16-JUN-2005 (First entry)
 ID ADY99903 standard; protein; 842 AA.
 AC ADY99903;
 XX Human codon-optimized HIV B Env protein.

KW env; viral replication; recombinant DNA; vector; vaccine; cancer;
KW infectious disease; HIV; hepatitis; variola virus infection;
KW immune stimulation; antimicrobial; viricide; anti-HIV; cytostatic;
KW antiinflammatory; hepatotropic; immunogenicity.

OS Homo sapiens.
XX Human immunodeficiency virus 1.
 PN WO2005028634-A2.
 XX 31-MAR-2005.
 PD 20-SEP-2004; 2004WO-US030849.
 PR 18-SEP-2003; 2003US-0504030P.
 XX (UYEM-) UNIV EMORY.
 PI Feinberg MND, Garber D;
 DR WPI: 2005-234126/26.
 DR N-PSDB; ADY99902.
 XX New recombinant modified vaccinia Ankara virus comprising first null

mutation in vaccinia gene, useful for treating or preventing viral infection (e.g. HIV, hepatitis and smallpox), and cancer.

PT PT XX
 PT XX
 PS Claim 69; SEQ ID NO 31; 324pp; English.

This invention relates to a novel recombinant modified vaccinia Ankara virus (rMVA). Specifically, it refers to the use of rMVA vectors in the development of vaccines to protect against cancer or infectious viral diseases such as HIV, hepatitis and smallpox. The present invention concerns introducing a null mutation (preferably a deletion) into a particular an exemplary gene is the vaccinia uracil DNA glycosylase gene. Additional vaccinia genes that can contain null mutations include, but are not limited to, IL1 beta receptor, A46R, IL-18BP, A41L and B3L. Accordingly, it provides a system for producing an appropriate vaccine that involves an immortalized, non-transformed avian fibroblast cell infected with the rMVA, where the cell is from a complementing cell line that is engineered to express the gene necessary for viral replication, such that the virus is able to propagate. Furthermore, the rMVA may include a heterologous nucleic acid sequence encoding an antigen or a fragment thereof derived from viral, animal or plant polynucleotides, for example this may include an antigen from the HIV virus, measles virus, SARS virus, influenza virus, malaria plasmodium, Bacillus, yellow fever virus, dengue flavivirus or the river blindness nematode. The rMVA also comprises a second heterologous nucleic acid sequence encoding a pro-apoptotic, anti-apoptotic or an immunomodulator operably linked to an early stage viral promoter. As such, the developed vaccine can be administered in a sufficient amount to effect an immune response in a host and exhibits antimicrobial, viricide, anti-HIV, cytostatic, antiinflammatory and hepatotropic activities. This polypeptide sequence is a human codon-optimized HIV-1 consensus protein sequence, encoded by an antigenic sequence of an MVA-based vector given in an exemplification of the invention.

XX Sequence 842 AA;
 Query Match 84.8%; Score 2947; DB 9; Length 842;
 Best Local Similarity 86.2%; Pred. No. 5.4e-158;
 Matches 558; Conservative 25; Mismatches 40; Indels 24; Gaps 5;

Qy 3 LWVTTYYGVPWKEATTTLFCASDAKAYDTAEAHNTWATHACVPTNPQEVVLENVENTNF 62
 Db 33 LWVTTYYGVPWKEATTTLFCASDAKAYDTAEAHNTWATHACVPTNPQEVVLENVENTNF 92
 Qy 63 NMWKNMVEQHED1ISLWDOSL1KPCVKLTPLCVTLNCTDLNTNTNTLNSIVVWEQ 122
 Db 93 NMWKNMVEQHED1ISLWDOSL1KPCVKLTPLCVTLNCTDL--RVAHTNTSSS---WET 146
 Qy 123 RGKGENRNCSPNITTSIRDVKQREYALFYKLDVPEPDNNKNTNTKYLINCNTSVITQ 182
 Db 147 MEKGEBIKNCSPNITTSIRDVKQREYALFYNLDVVPID-----MASYRLISNCNTSVITQ 199
 Qy 183 ACPKSFEPIPITHCPTGFALLKNDKKEFNGTGCTNVSTVQCHGIRPVVSTOLLNG 242
 Db 200 ACPKSFEPIPITHCPTGFALLKNDKKEFNGTGCTNVSTVQCHGIRPVVSTOLLNG 259
 Qy 243 SLAEENVIRSENFTNAKTTIVOLNVNSVBNCTRNNTKRTKRTLGPGRWYTGCILS 302
 Db 260 SLAEENVIRSENFTNAKTTIVOLNVNSVBNCTRNNTKRTKRTLGPGRWYTGCILS 319
 Qy 303 NTRQHCNCISRAQWNTLQIAATTREQFGNKTIAFNQSSGDPPEVMHSPNCGEFYC 362
 Db 320 DIRQHCNCISRAKWNNTLKV1K2IREQFGNKTIVPNQSSGDPPEVMHSPNCGEFYC 379
 Qy 363 NSTQLENSAVNTSNGTWSVTRKQDGTITLPCRIKQIINRWQVYKAMYALP1KGLI 422
 Db 380 NSTQLP-----TWNDTRKLNTGRNTLPCRIKQIINMWQEVKAMYAP1RQGI 429
 Qy 423 RCSSNTGLLILTRDQGENQTEITFPGGGDMRDWNRSELKYKTVKIEPLGVAP1KAR 482
 Db 430 RCSSNTGLLILTRDQKDTNGTEIFPGGGDMRDWNRSELKYKTVKIEPLGVAP1KAR 489
 Qy 483 RVVQREKRAVGMGLGAMFLGLGAAGSTMGATSMALTVQARQLLSGIVQQQNNLRAIKAQ

OS	Homo sapiens.	Db	1734	ACPKVSEPIPHYCAPAGFAILKNDKKENGTCPTNVSTVQCTHIGRPPVSTQLLNG	1793
XX	Human immunodeficiency virus 1.	Qy	243	SLAEEEVIRSENFTNAKTTIVQUNVSVEINCPENNHTRKRVTPGPRWYTGEILG	302
PN	WO2005028634-A2.	Db	1794	SLAEEEVIRSENFTNAKTTIVQUNVSVEINCPENNHTRKRVTPGPRWYTGEILG	1853
XX	31-MAR-2005.	Qy	303	NIROAHCNISRAQWNNTLQQATTREQFNKNTIAFNQSSGGDPRIVMISFNCGBEFFYC	362
PD		Db	1854	DIRQAHCNISRAKWNNTLQVIRKBRQFNKNTIVNQSSGDPRIVMISFNCGBEFFYC	1913.
PF	20-SEP-2004; 2004WO-US030849.	Qy			
XX		Db			
PR	18-SEP-2003; 2003US-0504030P.	Qy	363	NSTQLFNSAMVNTSNGTWSYTRKDTGDLITLPCKIQIINRQVKGAMYALPIKGLI	422
XX	(UYEM-) UNIV EMORY.	Db	1914	NSTQLF-----TWNDTRKLNTGRNTLPCRKQIINMNCQBVGKAMYAPPTRGQI	1963
PA		Qy	423	RCSSNTGLLITRDGGENOTTEIRPGGGDMRDWRSLEYKVKVKEPLGVARTKARR	482
XX		Db	1964	RCSSNTGLLITRDGGENDTETRPGGGDMRDWRSLEYKVKVKEPLGVARTKARR	2023
PT	WPI; 2005-354126/26.	Qy	483	RVVOREKRKAVGMLGFMFLGFLGAAGSTMGAATSMALTVQARQLLSGIVQOQNLLRAIAKQ	542
XX	DR-N-PSDB; AD399928.	Db	2024	RVVKERKAVGMLGFMFLGFLGAAGSTMGAASMTLVQARQLLSGIVQOQNLLRAIAEQ	2082
PS	New recombinant modified vaccinia Ankara virus comprising first null.	Qy			
PT	PT mutation in vaccinia gene, useful for treating or preventing viral	Db			
PT	infection (e.g. HIV, hepatitis and smallpox), and cancer.	Qy	543	OHLQLTWKGKOLQARIILVERYIKDQOLLGFCNSGKLICTTAAPVNAWSNKTLDQI	602
XX	Claim 69; SEQ ID NO 57; 324pp; English.	Db	2083	OHLQLTWKGKOLQARIILVERYIKDQOLLGFCNSGKLICTTAAPVNAWSNKTLDQI	2142
XX	This invention relates to a novel recombinant modified vaccinia Ankara	Qy	603	WNNMTWMEIDNTHYLITYLIESONQEKNQELLDKWAHL	649
CC	virus (rMVA). Specifically, it refers to the use of rMVA vectors in the	Db	2143	WNNMTWMEIDNTHYLITYLIESONQEKNQELLDKWAHL	2189
CC	development of vaccines to protect against cancer or infectious viral				
CC	diseases such as HIV, hepatitis and smallpox. The present invention				
CC	describes introducing a null mutation (preferably a deletion) into a				
CC	vaccinia gene that is necessary for replication of the rMVA, in				
CC	particular an exemplary gene is the vaccinia uracil DNA glycosylase gene.				
CC	Additional vaccinia genes that can contain null mutations include, but				
CC	are not limited to, IL1 beta receptor, A46R, IL-18BP, A41L and B3L.				
CC	Accordingly, it provides a system for producing an appropriate vaccine				
CC	that involves an immortalized, non-transformed avian fibroblast cell				
CC	infected with the rMVA, where the cell is from a complementing cell line				
CC	such that the virus is able to propagate. Furthermore, the rMVA may				
CC	include a heterologous nucleic acid sequence encoding an antigen or a				
CC	fragment thereof derived from viral, animal or plant polynucleotides, for				
CC	example this may include an antigen from the HIV virus, measles virus,				
CC	SARS virus, influenza virus, malaria plasmodium, tuberculosis Bacillus,				
CC	Yellow fever virus, dengue flavivirus or the river blindness nematode.				
CC	The rMVA also comprises a second heterologous nucleic acid sequence				
CC	encoding a pro-apoptotic, anti-apoptotic or an immunomodulator operably				
CC	linked to an early stage viral promoter. As such, the developed vaccine				
CC	can be administered in sufficient amount to effect an immune response				
CC	in a host and exhibits antimicrobial, virucide, anti-HIV, cytostatic,				
CC	antiinflammatory and hepatotoxic activities. This polypeptide sequence				
CC	is a human codon-optimized HIV-1 consensus fusion protein sequence,				
CC	encoded by an antigenic sequence of an MVA-based vector given in an				
CC	exemplification of the invention.				
XX	Sequence 2602 AA;	Qy	84.8%; Score 2947; DB 9; Length 2602;		
SQ	Best Local Similarity 86.2%; Pred. No. 1.4e-157;	Matches 558; Conservative 25; Mismatches 40; Indels 24; Gaps 5;			
Qy	3	LWVTVTVGVPWKEATTTLFCASDAKAYDTAAHNTWATHACVPTNPNPQEVLNTENF	62		
Db	1567	LWVTVTVGVPWKEATTTLFCASDAKAYDTAAHNTWATHACVPTDNPQEVLNTENF	1626		
Qy	63	NMKWNNMVQEHBEDIIISLWDLSLKPCVTLPCVTLNCNTLNTNTTIELSIIVWEQ	122		
Db	1627	NMKWNNMVQEHBEDIIISLWDLSLKPCVTLPCVTLNCNTL--RNATNTSSS---WET	1680		
Qy	123	RGKGENRCSNNTTSIRDQYRQEYALFYKUDPIDDKNNTNTTAKYRLINCNTSVITQ	182		
Db	1681	MFKGEIKNCSEWITSRDKYQKEYALFYNLDVWPID-----NASYRILISCTNSVITQ	1733		
Qy	183	ACPKVSEPIPHYCAPAGFAILKNDKKENGTCPTNVSTVQCTHIGRPPVSTQLLNG	242		

PS Disclosure; Fig 28A; 284pp; English.

XX The invention describes an isolated protein (I) selected from 106 fully defined 500-866 amino acid sequences given in the specification. Also CC described are: a nucleic acid comprising: a nucleotide sequence encoding CON6 HIV gp160 protein, subtype C ancestral HIV envelope protein, subtype C consensus HIV envelope protein, subtype C consensus HIV gag protein, subtype C consensus HIV nef protein, Group M consensus HIV protein, subtype A consensus HIV envelope protein, Group M consensus HIV gag protein, Group M consensus HIV pol protein, Group M consensus HIV gag protein, subtype C consensus HIV pol protein, subtype B consensus HIV gag protein, or subtype B consensus HIV envelope protein, where the nucleotide sequence comprises codons optimized for expression in human cells; a nucleotide sequence encoding (I); or a nucleotide sequence selected from 89 fully defined 633-2607 bp sequences given in the specification; a vector comprising the nucleic acid of (I); a composition comprising at least one protein or nucleic acid above and a carrier; and inducing an immune response in a mammal. The protein is a consensus or ancestral immunogen useful for inducing antibodies that neutralize a wide spectrum of HIV primary isolates and/or that induces a T cell response. This is the amino acid sequence of a HIV (CON-B) consensus gp140 env fusion protein.

XX Sequence 841 AA;

SQ Query Match 84.6%; Score 2939.5; DB 9; Length 841;

Best Local Similarity 86.1%; Pred. No. 1.4e-157; Indels 25; Gaps 7; Matches 557; Conservative 31; Nismatches 34;

Db 93 NMWKQNMVMEQNHEDITSLWQSLKECYKLTPLCVTLNCNTNTNLNTNTLSTIVWWEQ 122

Db 33 LMWTVYYGVGVWKEATTTLPCASDAKAYDTEARNWATHACVPTNPNPQEVLLENVNENF 62

Db 33 LMWTVYYGVGVWKEATTTLPCASDAKAYDTEHNWATHACVPTDPPNPQEVLLENVNENF 92

Qy 63 NMWKQNMVMEQNHEDITSLWQSLKECYKLTPLCVTLNCNTNTNLNTNTLSTIVWWEQ 122

Db 93 NMWKQNMVMEQNHEDITSLWQSLKECYKLTPLCVTLNCNTNTNLNTNTLSTIVWWEQ 122

Qy 123 RGKGMERNCSNNTISIRDKVQREVALFYKLDVEPDDIKNTNTNKYLINCNNTSIVTQ 182

Db 148 --RGEIKNCSEFNITSIRDKVQKEALFYKLDVVPIDN---DNTSYFLISCNNTSIVTQ 200

Qy 183 ACPKVSFEPIPHYCTPTGFALLKCNDFKFNGTGFCNTNVSTVQCTHGRPVYSTOLLING 242

Db 201 ACPKVSFEPIPHYCAPAGFAILKCNDFKFNGTGFCNTNVSTVQCTHGRPVYSTOLLING 260

Qy 243 SLAEEBVVISENFNTNAKTLIVQANVSEINCRPNNTTRKRVTLGPQRWVTTGELIG 302

Db 261 SLAEEBVVISENFNTDNAKTIVQLNESTVINCTRPNNTTRKRVTLGPQRWVTTGELIG 320

Qy 303 NIROAHCNISRAQWNTLQQATLIREQFGNKTIAFNQSGGDPEIVMFSNCGEFFYC 362

Db 321 DIROAHCNISRAKWNNTLROIKVKKLREQFGNKTIVFNQSGGDPEIVMFSNCGEFFYC 380

Qy 363 NSTOLFNSAWNTVTSNGTWYTRKQKDITLPCRIKQIOLINRMQVYGHAMYALPIKGII 422

Db 381 NTQLENSTW---NGTWN----NTEGNITLPCRIKQIOLINWQMVEGVGHAMYAPPICGI 430

Qy 423 RCSSNITGGLITRDGGGENOTTEIRPGQGDMDRNWRSLEYKVKVTKRBLPLGVAPTKKAR 482

Db 431 RCSSNITGGLITRDGG--NNNETEIRPGQGDMDRNWRSLEYKVKVTKRBLPLGVAPTKKAR 488

Qy 483 RVVQREKRKAVGMLGAMFLGFLGAAGSTMGATSMALTVQRQLISIVQQQNLLRAIKQ 542

Db 489 RVVQREKRKAVG-IGAMFLGFLGAGSTMGASMTLVQRQLLSIVQQQNLLRAIKQ 547

Qy 543 QHLLQLTWIGKIKOLOARI LAVERLYLKDQQLLGNGC SGKLICITAVPNASWSNKTLDQI 602

Db 548 QHLLQLTWIGKIKOLOARI LAVERLYLKDQQLLGNGC SGKLICITAVPNASWSNKSLSDBI 607

Qy 603 WNNMTWEMWEIRDNTYTHLTYLTLIESQNOEQNEQELLDKMASI 649

Db 608 WDNTMTWEMWEIRDNTYTHLTYLTLIESQNOEQNEQELLDKMASI 654

PS Disclosure; Fig 28A; 284pp; English.

XX The invention describes an isolated protein (I) selected from 106 fully

CC defined 500-866 amino acid sequences given in the specification. Also

CC described are: a nucleic acid comprising: a nucleotide sequence encoding

CC CON6 HIV gp160 protein, subtype C ancestral HIV envelope protein, subtype C consensus HIV envelope protein, subtype C consensus HIV gag protein, subtype C consensus HIV nef protein, Group M consensus HIV protein, subtype C consensus HIV pol protein, Group M consensus HIV gag protein, subtype C consensus HIV nef protein, Group M consensus HIV pol protein, Group M consensus HIV gag protein, or subtype C consensus HIV envelope protein, where the

CC nucleotide sequence comprises codons optimized for expression in human

CC cells; a nucleotide sequence encoding (I); or a nucleotide sequence

CC selected from 89 fully defined 633-2607 bp sequences given in the

CC specification; a vector comprising the nucleic acid of (I); a composition

CC comprising at least one protein or nucleic acid above and a carrier; and

CC inducing an immune response in a mammal. The protein is a consensus or

CC ancestral immunogen useful for inducing antibodies that neutralize a wide

CC spectrum of HIV primary isolates and/or that induces a T cell response.

XX This is the amino acid sequence of HIV (CON-B) env protein.

SQ Sequence 841 AA;

Qy 3 LMWTVYYGVGVWKEATTTLPCASDAKAYDTEARNWATHACVPTNPNPQEVLLENVNENF 62

Db 33 LMWTVYYGVGVWKEATTTLPCASDAKAYDTEHNWATHACVPTDPPNPQEVLLENVNENF 92

RESULT 15
AD207794 ID AD207794 standard; protein; 841 AA.XX ID AD207794;
AC AC
DT 16-JUN-2005 (first entry)

XX HIV CON-B env protein.

XX KW anti-HIV; Immunostimulant; immune stimulation; HIV infection; infection;

CC CON-B; env; envelope.

XX Human immunodeficiency virus.

XX OS WO005028625-A2.

XX PD 31-MAR-2005.

XX PF 17-SEP-2004; 2004WO-US030397.

XX PR 17-SEP-2003; 2003US-053460P.
PR 27-AUG-2004; 2004US-0504722P.

XX PA (UVDU-) UNIV DUKE.

PA (KORBER/) KORBER, B. T.

PA (HANN/) HANN, B. H.

PA (SHAW/) SHAW, G. M.

PA (KOTHE/) KOTHE, D.

PA (LIYY/) LI, Y. Y.

PA (DECKER/) DECKER, J.

XX PI Korber, BT, Hahn, BH, Shaw, GM, Kothe, D, Li, YY, Decker, J;

PI Haynes, BF, Gao, F, Liao, H;

XX XX DR WPI, 2005-242571/25.

DR N-PSDB; AD207796.

XX PT New isolated consensus or ancestral immunogenic proteins, useful for

PT inducing antibodies that neutralize a wide spectrum of human

PT immunodeficiency virus (HIV) primary isolates and/or that induces a T

PT cell response.

XX PS Claim 66; Fig 44A; 284pp; English.

XX The invention describes an isolated protein (I) selected from 106 fully

CC defined 500-866 amino acid sequences given in the specification. Also

CC described are: a nucleic acid comprising: a nucleotide sequence encoding

CC CON6 HIV gp160 protein, subtype C ancestral HIV envelope protein, subtype

CC C consensus HIV envelope protein, subtype C consensus HIV gag protein,

CC subtype C consensus HIV nef protein, Group M consensus HIV envelope

CC protein, subtype A consensus HIV envelope protein, Group M consensus HIV

CC gag protein, Group M consensus HIV pol protein, Group M consensus HIV nef

CC protein, subtype C consensus HIV pol protein, subtype B consensus HIV gag

CC protein, or subtype B consensus HIV envelope protein, where the

CC nucleotide sequence comprises codons optimized for expression in human

CC cells; a nucleotide sequence encoding (I); or a nucleotide sequence

CC selected from 89 fully defined 633-2607 bp sequences given in the

CC specification; a vector comprising the nucleic acid of (I); a composition

CC comprising at least one protein or nucleic acid above and a carrier; and

CC inducing an immune response in a mammal. The protein is a consensus or

CC ancestral immunogen useful for inducing antibodies that neutralize a wide

CC spectrum of HIV primary isolates and/or that induces a T cell response.

XX This is the amino acid sequence of HIV (CON-B) env protein.

SQ Sequence 841 AA;

Qy 3 LMWTVYYGVGVWKEATTTLPCASDAKAYDTEARNWATHACVPTNPNPQEVLLENVNENF 62

Db 33 LMWTVYYGVGVWKEATTTLPCASDAKAYDTEHNWATHACVPTDPPNPQEVLLENVNENF 92

Qy 3 LMWTVYYGVGVWKEATTTLPCASDAKAYDTEHNWATHACVPTDPPNPQEVLLENVNENF 92

Db 33 LMWTVYYGVGVWKEATTTLPCASDAKAYDTEHNWATHACVPTDPPNPQEVLLENVNENF 92

Query Match 84.3%; Score 2927.5; DB 9; Length 841;
Best Local Similarity 85.9%; Pred. No. 6.8e-157;
Matches 556; Conservative 31; Mismatches 35; Indels 25; Gaps 7;

3 LMWTVYYGVGVWKEATTTLPCASDAKAYDTEHNWATHACVPTDPPNPQEVLLENVNENF 62

Db 33 IWWTVVYGVPKBEATTLFGASDAKAYDTVEHNVWATHACRYPTDNPQESTVLENNTENP 92
 Qy 63 NWKNNRNVEQMEBDIISLWDQSUKPCVTLTLCVTNCTDINTANTNTPELSITIVVWBQ 122
 Db 93 NWKNNRNVEQMEBDIISLWDQSUKPCVTLTLCVTNCTDLMNNTNTT--IIYRW- 147
 Qy 123 RGRGEMRNCSENNTTSIRDKVOREYALFYKLDEPIDDNQNTNTNTKYRLINCNTSVITQ 182
 Db 148 -RGEIIXNCSPNITSIRDKVOREYALFYKLDEVIDVVPDN---DNTSYRLISCNSTSVITQ 200
 Qy 183 ACPKVSPERPIPHYCPTGPALLKCNDKFKNGTGPCTNVSITYQCHTGIRPVSTOLLING 242
 Db 201 ACPKVSPERPIPHYCAGFAILKCNDKFKNGTGPCTNVSITYQCHTGIRPVSTOLLING 260
 Qy 243 SLAEEETVIRSENFTINAKTIVOLNESEINCTRPNNTKTRVTLGPGRWYTGTIGLG 302
 Db 261 SLAEEETVIRSENFTDANKTIVOLNESEINCTRPNNTKSHIGPGRAPHYTGIGLG 320
 Qy 303 NIRQAHCNISRAQWNNTLQIAUTTREQFGNTIAFNQSSGDPETVMHSFNCGEFFYC 362
 Db 321 DIRQAHENISRAKWNNTLKQIVKRQLEQFGNTIVVNQSSGDPETVMHSFNCGEFFYC 380
 Qy 363 NSTOLFNSAWNNTSNGTWSVTRKOKDGTDTLPCKQIINRQVUGKAMYALPKGLI 422
 Db 381 NTTOLFNSTW---NGTW-----NTEGNLTLPCKQIINMWOEVGKAMYAPPTRQD 430
 Qy 423 RCSSNTGLLLPRDGGBENQTEIFRGGGDMDNTRSELKYKVKEPLGVAPTKAR 482
 Db 431 RCSSNTGLLLTRDGG--NNTEIFRGGGDMDNTRSELKYKVKEPLGVAPTKAR 488
 Qy 483 RVVQREKAVGMGLGAMEFLGLGAAGSTMAGTSMALTYQAROLLG3TIVQQONNLRAIKAQ 542
 Db 489 RVVQREKAVG-IGAMFLGFLGAAGSTMGAASMTLTVQAROLLG3TIVQQONNLRAIEAQ 547
 Qy 543 QHLLQLTWGIKOLQARILAYERVLKDQQLGPAGCSGKLICCTAVPNMASWSNKTLDQI 602
 Db 548 QHLLQLTWGIKOLQARILAYERVLKDQQLGPAGCSGKLICCTAVPNMASWSNKSLSDBI 607
 Qy 603 WDNMTTNEWDREIDNTHLITLIESQNQOERNOELQLQDJKWASL 649
 Db 608 WDNMTTNEWERBIDNTSLLTLYLIESQNQOEKNEQELLEDJKWASL 654

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Db	261	LNGSLABEIVIRSENFTNDAKTIIVHLLNESVEINCTRPNVNRRHHIIGPGRFY-TG	319	Qy	363	NSTQLFNSAWNVTSGNTMSVTRKOKDGTIDLIITLPCRKIQOIINWQVVGKAMYALPIKGJL	422
Qy	299	EILGNIROAHCNISRAQWNNTLQQIATTIREQFNKTIAPNOSSGGDPVVMSFNCGB	358	Db	381	NSTQLFNSAWNNTGEGT-----NNTEGNTITLPCRKIQOINNMQEVGKAMYAPPIRGQI	434
Db	320	EIRGNTRQAHCNISRAKWNNTLQQIATTIREQFNKTIENHSSCGDPVVTSFNCGB	379	Qy	423	RCSSNITGGLLTRDGGGENOTTEIFPRGGDMRDNWRSLEYKVKTCBPLGVAPTKAKR	482
Qy	359	FYCNSTQLFNSAWNVTSGNTWSVTRKQDGTIDLIITLPCRKIQOINNMQEVGKAMYAFLI	418	Db	435	RCSSNITGGLLTRDGGGENOTTEIFPRGGDMRDNWRSLEYKVKTCBPLGVAPTKAKR	494
Db	380	FPCDSTSQTQLFNSAWNVTSGNTISTEGNNNTBEENGDTITLPCRKIQOINNMQVGKAMYAFLI	438	Qy	483	RVYOREKRAVGMTGAMFLGFLGAAGSTMATSMALTYQAROLISGIVOCQNNILRATAKQ	542
Qy	419	KGLTRCSSNTGGLLTDGGGENOTTEIFPRGGDMRDNWRSLEYKVKTCBPLGVAPT	478	Db	495	RVYOREKRAVG-IGAVFLGFLGAGSTMCASHTLVQARLISGIVOCQNNILRATAEQ	553
Db	439	GQIICRSSNTGGLLTDGGENSSREEIFPRGGDMRDNWRSLEYKVKTCBPLGVAPT	498	Qy	543	QHLQLTWGKIKOLQARI LAVERYLKDQQLGTMGSGKLICHTAVPNASMSNKTLDOI	602
Qy	479	KAKRKYVQREKRAVGMLGAMFLGFLGAAGSTMATSMALTYQAROLISGIVOCQNNILRFA	538	Db	554	QRMLQLTWGKIKOLQARI LAVERYLGDQQLGTMGSGKLICHTAVPNASMSNKLSLRI	613
Db	499	KAKRKYVQREKRAVGMLGAMFLGFLGAAGSTMATSMALTYQAROLISGIVOCQNNILRFA	558	Qy	603	WNNNTWMDREIDNTYTHLYTLLIESONQQEKNQQLDQWLDSL	649
Qy	539	IKAQHLLQLTWGMKIKOLQARI LAVERYLKDQQLGTMGASLSTTVQAROLISGIVOCQNNILRFA	598	Db	614	WNNNTWMDREIDNTYSEIYLIESONQQEKNQQLDQWLDSL	660
Db	559	IEAQHLLQLTWGMKIKOLQARI LAVERYLKDQQLGTMGSGKLICHTAVPNASWSNKS	618				
		RESULT 5					
		T12016					
		envelope glycoprotein - human immunodeficiency virus type 1 (strain SC14.3)					
		C;Species: human immunodeficiency virus type 1, HIV-1					
		C;Accession: T12016					
		C;Accession: T12016					
		R; McCutchan, F.E.; Sanders-Buell, B.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.					
		AIDS Res. Hum. Retroviruses 14, 329-337, 1998					
		A;Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S					
		A;Reference number: Z17379; MUID:98178716; PMID:9519894					
		A;Status: preliminary; translated from GB/EMBL/DBJ					
		A;Molecule type: DNA					
		A;Cross-references: UNIPROT:O41883; UNIPARC:UPI0000101F2; EMBL:U90934; NID:92351783; P1					
		A;Genetics:					
		C;Superfamily: type E retrovirus env polyprotein					
		Query Match 81.7%; Score 2837; DB 2; Length 852;					
		Best Local Similarity 83.1%; Pred. No. 3.7e-200;					
		Matches 541; Conservative 35; Mismatches 53; Indels 22; Gaps 8;					
		Query 3 LWVTTYYGVPWKWEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNOBVVLENTEF					
		Db 33 LRVTTYYGVPWKWEATTTLFCASDAKAYDTEAHNVWATHACVPTDPNQEVVLLKNTENF					
		Qy 63 NMWKNMVYEQMHED1ISLDOSLKPCKVLUPLCYTLLCDLNTNNNTTELSLIVVWEQ					
		Db 93 NMWKNMVYEQMHED1ISLDQSLKPCKVLUPLCYTLLCDLNTNNNTTELSLIVVWEQ					
		Db 123 RG---KGEMRNCSFNITTSIRDKVQREYALFYKLDVEPIDDNNKNTNTKYRJINCNTS					
		Db 199 VITQCPKVSFEPIHYCPTPGFALLKCNDDKKGNTGCTNVSTVQOCTHGIRPVSTQL					
		Qy 239 LLNGSLAEEEVIRSENFTNDAKTYLQKVEALFYKLDVWID--NTT--TSYRLJINCNTS					
		Db 144 NGGGREGGEKNCSSNITRIGRNKQKEALFYKLDVWID--NTT--TSYRLJINCNTS					
		Db 179 VITQCPKVSFEPIHYCPTPGFALLKCNDDKKGNTGCTNVSTVQOCTHGIRPVSTQL					
		Db 199 VITQCPKVSFEPIHYCPTPGFALLKCNDDKKGNTGCTNVSTVQOCTHGIRPVSTQL					
		Qy 259 LLNGSLAEEEVIRSENFTNDAKTYLQKVEALFYKLDVWID--NTT--TSYRLJINCNTS					
		Db 299 EILGNIROAHCNISRAQWNNTLQQIATTIREQFNKTIAPNOSSGGDPETVMSFNCGG					
		Db 319 AIGGIROAHCNISRAQWNNTLQQIATTIREQFNKTIAPNOSSGGDPETVMSFNCGG					
		Db 359 FPCNSTMPLNSAWNVTSGNTMSVTRKQDGTIDLIITLPCRKIQOINRWQVVGKAMYALPI					
		Db 379 FFYCNTTFLKFNSTW-MFENNTWNDEDTGNG-TTLPCRQKQIINRWQVVGKAMYAPPI					
		Db 419 KGLRCSSNTGLLTRDGGENQTE1FRPGGGMDRNWSLRYKVKVIEPLGVAPT					

RES048 envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Accession: T09448 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 R; Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Royanagi, Y.; Namazie, A; Reference number: Z16673
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-847 <PAN>
 A;Cross-references: UNIPROT:Q75760; UNIPARC:UPI000010516; EMBL:U63632; NID:91465777; PI
 C;Genetics:
 A;Gene: env
 C;Superfamily: type E retrovirus env polyprotein

Query Match 82.0%; Score 2849.5 ; DB 2; Length 847;
 Best Local Similarity 82.8%; Pred. No. 4.4e-201;
 Matches 536; Conservative 40; Mismatches 52; Indels 19; Gaps 4;

Qy 3 LWVTTYYGVPWKWEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNOBVVLENTEF

Db 63 NMWKNMVYEQMHED1ISLDOSLKPCKVLUPLCYTLLCDLNTNNNTTELSLIVVWEQ

Db 93 NMWKNMVYEQMHED1ISLDQSLKPCKVLUPLCYTLLCDLNTNNNTTELSLIVVWEQ

Db 123 RG---KGEMRNCSFNITTSIRDKVQREYALFYKLDVEPIDDNNKNTNTKYRJINCNTS

Db 199 VITQCPKVSFEPIHYCPTPGFALLKCNDDKKGNTGCTNVSTVQOCTHGIRPVSTQL

Qy 239 LLNGSLAEEEVIRSENFTNDAKTYLQKVEALFYKLDVWID--NTT--TSYRLJINCNTS

Db 259 LLNGSLAEEEVIRSENFTNDAKTYLQKVEALFYKLDVWID--NTT--TSYRLJINCNTS

Qy 323 RGGGENRNCSPNITTSIRDKVQREYALFYKLDVEPIDDNNKNTNTKYRJINCNTS

Db 379 -ERGIIKNCSPNITTSIRDKVQREYALFYKLDVWID--NTT--TSYRLJINCNTS

Qy 183 ACPKVSFEPIHYCPTPGFALLKCNDDKKGNTGCTNVSTVQOCTHGIRPVSTOLLING

Db 201 ACPKVSFEPIHYCAGPAFLKCNDDKKGNTGCTNVSTVQOCTHGIRPVSTOLLING

Qy 243 SLAEEEVIRSENFTNDAKTYLQKVEALFYKLDVEPIDDNNKNTNTKYRJINCNTS

Db 261 SLAEEEVIRSDNFTNDAKTYLQKVEALFYKLDVEPIDDNNKNTNTKYRJINCNTS

Db	436	RQIIRCSNITGILLTRG3NNSTNETPRGGDMRDWRSELYKVKVKBPLGVAPT	495	QY	543	OHLQLTYWGIKOLQARILAVERYLKDQQLLGFWGCGKLICITTAVPWNASNSNKTLDDQI	602				
Qy	479	KAKRVRVQREKRAVGMLGAMFLGFGAAGSTMGAATMGTSMALTVQARQLSCLIVQQNNLLRA	538	Db	554	QRMUQLTYWGIKOLQARILAVERYLGDQQLLGFWGCGKLICITTAVPWNASNSNKTLDDRI	613				
Db	496	KAKRVRVQREKRAVGMLGAMFLGFGAAGSTMGAATVLTQARQLSCLIVQQNNLLRA	554	QY	603	WNNNTWWMDREIDNTYLIYTIESONQEQEQQNELLQDQWL	649				
Qy	539	IKAQHLLQLTWGIKOLQARILAVERYLKDQQLIGWGCGKLICITTAVPWNASNSNKTT	598	Db	614	WNNNTWWEREDNTSEIYTIESONQEQEQQNELLQDQWL	660				
Db	555	IEAQHLLQLTWGIKOLQARILAVERYLKDQQLIGWGCGKLICITTAVPWNASNSNKTS	614	RESULT 7							
Qy	599	LDOIWNNTMWEDEIDNTYLIYTIESONQEQEQQNELLQDQWL	649	env polyprotein - human immunodeficiency virus type 1 (isolate BR)							
Db	615	LDCTWNNTMWEDEIDNTSLISLIESONQEQEQQNELLQDQWL	665	N;Alternate names: coat polyprotein							
RESULT 6								C;Contains: coat protein gp41			
C;Species: human immunodeficiency virus type 1, HIV-1		C;Species: human immunodeficiency virus (HIV-1)		C;Accession: A31667	A;Note: host Homo sapiens (man)	C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004		R;Anand, R.; Thayer, R.; Srinivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; Dandekar, S			
C;Accession: S13289		C;Title: Biological and molecular characterization of human immunodeficiency virus type 1, HIV-1		C;Accession: A31667	A;Reference number: A94389; MUID:89085613; PMID:2789516						
C;Accession: S13289		A;Molecule type: DNA		A;Accession: A31667	A;Residues: 1-852 <AN>						
R;O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Diagne, A.; Idler, K.; Zack, J.A.		C;Superfamily: type E retrovirus env polyprotein		C;Cross-references: UNIPROT:PI12488; UNIPARC:UPI0000174A36							
Nature 348, 69-73, 1990		C;Keywords: capsid protein; coat protein; polyprotein; transmembrane protein		C;Keywords: capsid protein; coat protein; polyprotein; transmembrane protein							
A;Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120		F;1-516/Product: coat protein gp120 #status predicted <CP1>		F;1-517-852/Product: coat protein gp41 #status predicted <CP2>							
A;Accession: S13289											
A;Status: preliminary											
A;Molecule type: DNA											
A;Residues: 1-847 <OBR>											
A;Cross-references: UNIPROT:Q75760; UNIPARC:UPI000017861B											
C;Superfamily: type E retrovirus env polyprotein											
Query Match Score 81.1%; DB 1; Length 852;								C;Best Local Similarity 81.1%; Pred. No. 1-2e-18;			
Matches 528; Conservative 53; Mismatches 43; Indels 31; Gaps 7;								C;Score 2816.5; DB 1; Length 852;			
Query Match Score 81.6%; DB 2; Length 847;								C;Best Local Similarity 80.6%; Pred. No. 1-2e-18;			
Matches 534; Conservative 39; Mismatches 55; Indels 19; Gaps 4;								C;Score 2836.5; DB 2; Length 847;			
Qy	3	LWVTVYYGPVWKKEATTTCFCASDAKAYTDEAHNVATHACVPTNPQEVVLENTEFN	62	Qy	3	LWVTVYYGPVWKKEATTTCFCASDAKAYTDEAHNVATHACVPTNPQEVVLENTEFN	62	Db	34	LWVTVYYGPVWKKEANTTLCFCASDAKAYTDEAHNVATHACVPTDPNPQELVNGNTENF	93
Db	33	LWVTVYYGPVWKKEATTTCFCASDAKAYTDEAHNVATHACVPTNPQEVVLENTEFN	92	Qy	63	NMWKNNVMEQMHDIDIISLWQSLKPCVKLTPLCVYLNCTDLNTNTNTTELISIIVVWEQ	122	Db	94	NMWKNDVMEQMHDIDIISLWQSLKPCVKLTPLCVYLNCTDLNCHDWFATNSNS-----	143
Qy	63	NMWKNNVMEQMHDIDIISLWQSLKPCVKLTPLCVYLNCTDLNTNTNTTELISIIVVWEQ	122	Db	95	RGK---GEMRNSPNTTSIRDVKOREYALFYKLVIDPDDNNTNTKYRLINGNTS	178	Db	123	RGK---GEMRNSPNTTSIRDVKOREYALFYKLVIDPDDNNTNTKYRLINGNTS	178
Db	93	NMWKNNVMEQMHDIDIISLWQSLKPCVKLTPLCVYLNCTDLNTNTNTDSEGTM-----	146	Qy	123	RGK---GEMRNSPNTTSIRDVKOREYALFYKLVIDPDDNNTNTKYRLINGNTS	178	Db	144	-GMMEGEGEMRNSPNTTSIRDVKOREYALFYKLVIDPDDNNTNTKYRLINGNTS	199
Qy	123	RGK---GEMRNSPNTTSIRDVKOREYALFYKLVIDPDDNNTNTKYRLINGNTS	182	Db	147	-ERGEIKNSPNTTSIREDEVQKLYFKLDVIPDN----NNTSYRLISCDTSVITQ	200	Qy	179	VTOACPKVSPEPIP HYCPTGFAILKCNDFGKPTCINTVSTYQCTHGTGTPVYSTQL	238
Db	147	-ERGEIKNSPNTTSIREDEVQKLYFKLDVIPDN----NNTSYRLISCDTSVITQ	200	Db	183	ACPKVSPEPIP HYCPTGFAILKCNDFGKPTCINTVSTYQCTHGTGTPVYSTQL	242	Db	200	VITQACPKVTPEPIP HYCPTGFAILKCNDFGKPTCINTVSTYQCTHGTGTPVYSTQL	259
Qy	183	ACPKVSPEPIP HYCPTGFAILKCNDFGKPTCINTVSTYQCTHGTGTPVYSTQL	242	Db	201	ACPKVSPEPIP HYCPTGFAILKCNDFGKPTCINTVSTYQCTHGTGTPVYSTQL	260	Qy	239	LINGSLABEEVTRSEFTNNNAKTTIYOLNVESEINTRPNHTRKVLGFWGWWTTG	298
Db	201	ACPKVSPEPIP HYCPTGFAILKCNDFGKPTCINTVSTYQCTHGTGTPVYSTQL	260	Db	260	LINGSLABEEVTRSEFTNNNAKTTIYOLNVESEINTRPNHTRKVLGFWGWWTTG	319	Db	320	Q1GDRRAHCNLSRKWENLTKQITVNLKTFQKNKTVFNRSSGGDEIWHNSFCGGE	379
Qy	243	SLABEEVVRSENFTNNNAKTTIYOLNVESEINTRPNHTRKVLGFWGWWTTG	302	Qy	303	SLABEEVVRSENFTNNNAKTTIYOLNVESEINTRPNHTRKVLGFWGWWTTG	362	Qy	359	FFCNCNSTOLENSAW-NVTSNGTWSTVTRKQDKDTLTPCRKQIINRQWVYQKGAMYAL	416
Db	261	SLABEEVVRSENFTNNNAKTTIYOLNVESEINTRPNHTRKVLGFWGWWTTG	320	Db	321	SLABEEVVRSENFTNNNAKTTIYOLNVESEINTRPNHTRKVLGFWGWWTTG	380	Db	380	FFFCCNTTQLENSTWYRNTGNNT-----EGNSPITLPCRKQIINNMWQEVGAMYAP	431
Qy	303	SLABEEVVRSENFTNNNAKTTIYOLNVESEINTRPNHTRKVLGFWGWWTTG	320	Qy	381	PIGLIROSNTGNTLITRDGGCENQT--TEFRPGGDMRDWRSELYKVKVKEPLG	474	Qy	417	PIGLIROSNTGNTLITRDGGCENQT--TEFRPGGDMRDWRSELYKVKVKEPLG	474
Db	321	SLABEEVVRSENFTNNNAKTTIYOLNVESEINTRPNHTRKVLGFWGWWTTG	380	Db	432	PIRGQKCSNSITGLLITRDGGCENQT--TEFRPGGDMRDWRSELYKVKVKEPLG	491	Qy	492	VAPTKRVRVQEKRAVG-LGALFLPFLGAGSTMAASMTLVQARLLSGVQVOQNN	550
Qy	363	SLABEEVVRSENFTNNNAKTTIYOLNVESEINTRPNHTRKVLGFWGWWTTG	422	Qy	435	RCSSNTGILITRDGGCENQT--TEFRPGGDMRDWRSELYKVKVKEPLG	494	Qy	535	LLRAIAQHQHLLQTTWYKIKOLQARILAVERYLKDQQLLGFWGCGSKLICITTAVPWNASNSNKTLDDQI	594
Db	381	SLABEEVVRSENFTNNNAKTTIYOLNVESEINTRPNHTRKVLGFWGWWTTG	434	Db	495	RCSSNTGILITRDGGCENQT--TEFRPGGDMRDWRSELYKVKVKEPLG	553	Db	495	VVOREKRAVG-IGAVFLGFLGAGSTMAASMTLVQARLLSGVQVOQNN	594

Qy	422	IRCSSNITGILLLTRGG-----GENOTTB1FRPGGGDMRDNRSELYKVKVKBPLGVA	476	360	FYCNSTOLENSAWNTSNGTWSYTRKQKDGT-DIITLPCRIQOINRNOVGYKAMYALPI	418
Db	444	IRCSSNITGILLLTRGGNTNNNSIEFRPGGDMRDNRSELYKVKVKBPLGVA	503	383	FYCNSTQLENSTW--FNSTWSYGNSNTTEGSDTTLPCRIQINMDEVGKAMYALPI	439
Qy	477	PTKAKRVRVOREKRAVGMIGAMPLGLGAGSTMGCATSMALTYQAROLLSGIYQQNNL	536	419	KGLJRCSSNITGILLLTRGGGENOTEI FRPGGGDMRDNRSELYKVKVKBPLGVAFT	478
Db	504	PTRAKRVRVOREKRAV-IGAVFLGLGAGSTMGAATLTYQAROLLPGIYQQNNL	562	440	SGQJRCSSNITGILLLTRGGNSNNEIFRPGGGDMRDNRSELYKVKVKBPLGVAFT	499
Qy	537	RAIAQOHLQLLTWIKIQLQARLAVERTLKDQQLLGWGSGLICHTAVPMNASIN	596	479	KAKRVRVOREKRAVGLAMFLGPLGAGSTMGCATSMALTYQAROLLSGIYQQNNLRA	538
Db	563	RAIDQQLQLLTWIKIQLQARLAVERTLKDQLMGWCSCXPCTAVPMNTNSN	622	500	KAKRVRVOREKRAVG-IGAFLGFLGANGSTMGAASMTLTVQAROLLSGIYQQNNLRA	558
Qy	597	KTLDDQWNNTWMENDRETNYTHLJYTJBESONQEQKQNLQLQDQWASL	649	539	IKAQHLLQLTWIKIQLQARLAVERTLKDQQLLGNGCSGKLICCTAVPMNTNSRT	598
Db	623	RSFNE1WDNTWMEMBREINNYTLYNLIBESONQEQRNEQDLALDRDSL	675	559	IEAQHLLQLTWIKIQLQARLAVERTLKDQQLLGNGCSGKLICCTAVPMNTNSKS	618
Qy	599	LDOQIWNNTWMENDRETDNYTHLJYTJBESONQEQKQNLQLQDQWASL	649	619	LEQIWNNTWMEMBREINNYTSLIHSLIESQNQERNEQELLEDQWASL	669
Db						
RESULT 12						
VCUJH3 env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)						
N;Alternate names: coat polyprotein						
C;Species: human immunodeficiency virus type 1, HIV-1						
A;Note: host Homo sapiens (man)						
C;Accession: A03973						
R;Ratner, L.; Haseltine, W.; Patarca, R.; Starcich, B.; Josephs, S.F.; Dorzner, J.; Papas, T.S.; Ghayeb, J.; Gallo, R.C.; Wong-Staal, F.						
Nature 313, 277-284, 1985						
A;Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.						
A;Reference number: A93353; MUID:85111123; PMID:2578615						
A;Accession: A03973						
A;Residues: 1-856 <RAT>						
A;Cross-references: UNIPROT:P03375; UNIPARC:UPI000012A010; GB:M15654; GB:K02008; GB:K020						
C;Genetics:						
A;Gene: env						
C;Superfamily: type B retrovirus env polyprotein						
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein						
F;1-30/Domain: signal sequence #status predicted <SIG>						
F;51-511/Product: capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein						
F;512-856/Product: exterior membrane glycoprotein #status predicted <EXT>						
F;88-136,141-156,160,186,197,230,234,241,262,276,289,295,301,312,319,356,386-392,397,406						
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicted						
Query Match Score 2805.5%; DB 1; Length 856;						
Best Local Similarity 82.8%; Pred. No. 6-4e-198; Indels 19; Gaps 9;						
Matches 539; Conservative 35; Mismatches 58;						
Qy	3	LWVTTYYGPVWKBEATTLFCASDAKAYDTDEAHNVWATHACVPTNPNEPVVLENTE	62	Query Match Score 2799.5%; DB 1; Length 856;		
Db	34	LWVTTYYGPVWKBEATTLFCASDAKAYDTDEAHNVWATHACVPTNPQEVVLYNTEN	93	Best Local Similarity 82.5%; Pred. No. 2.1e-197; Indels 59; Gaps 9;		
Qy	63	NMWKNNMVEQMHEDD1ISLWQDOSLKEPLCVCYKTDLNTNTNTTELSTIVVWEQ	122	Matches 537; Conservative 36; Mismatches 59;		
Db	94	NMWKNDMVEQMHEDD1ISLWQDOSLKEPLCVCYKTDLNTNTSSGRMVE-150	150			
Qy	123	RKGEMRNCNSPNITSIIRDVKQREYALFYKLDVPEPDIDRNNTNTCYLINCTSVT	182			
Db	151	-KGEIKNCNSPNITSIIRDVKQREYAFYKLDPIDN---DTTSYLTSCNTSVT	203			
Qy	183	ACPKVSFEPIPPIHYCTPGEFALLKNDKENGTCPTCNVYSTQCHGIRPVVSTOLLING	242			
Db	204	ACPKVSFEPIPPIHYCAPAFALLKNDKENGTCPTCNVYSTQCHGIRPVVSTOLLING	263			
Qy	243	SLAEEVVVISSENFTNNAKTIIVQLNVSEINCRPNTTRK-RVTLGPRWYTTGEI	300			
Db	264	SLAEEVVVISSENFTNNAKTIIVQLNVSEINCRPNTTRK-RVTLGPRWYTTGEI	323			
Qy	301	LGNTIQAHCNISRAQWNNTLQIATLREQFG-NKTIATPQSSGDPETVMHSNCGEF	359			
Db	324	-GNRMOAHCNISRAKWNNTLKQIDSKEOFGNNTIIPKQSSGDPBVTHSFNCGEF	382			
Qy	301	LGNTIQAHCNISRAQWNNTLQIATLREQFG-NKTIATPQSSGDPETVMHSNCGEF	359			

Db	324 -GNNRQAHCNISRAKWNNTLKOIDSKLRFQFGNNTKTIIFQSSGGDPETVTHSFNCGGF	382	Qy	298 GBLLGNIROQAHCNISRAQWNNTLQQIATTLREQFG-NKTIAPNQSSGGDPETVMSFNCG	356
Qy	360 FYNCSNTOFLNSAWNTSNGTWSVTRKOKTG-DLTLPCKQJINRNOVYKGAMYALP	418	Db	326 GKI-GNMROQAHCNISRAKWNNTLQIAASKLRQGPNKTTIKQSSGGDPETVTHSFNCG	384
Db	383 FYNCSNTOLNSTW--FNSTWSTEGSNTTEGSDTITLPERIKOQINRNOVYKGAMYAPP	439	Qy	357 GPFYCNCNSTOLFNSAWNTSNGTWSVTRKOKTG-DLTLPCKQJINRNOVYKGAMYA	415
Qy	419 KGLIRCSSNTGSLITRDGGENOTTEIIRPGGDMRNWSLSELYKVKTEBPLGVAPT	478	Db	385 GPFYCNCNSTOLFNSTW--FNSTWSTEGSNTTEGSDTITLPERIKOQJINRNOVYKGAMYA	441
Db	440 SGQRCSSNTGSLITRDGGENOTTEIIRPGGDMRNWSLSELYKVKTEBPLGVAPT	499	Qy	416 LPIKGILPCSSNTGSLITRDGGENOTTEIIRPGGDMRNWSLSELYKVKTEBPLGV	475
Qy	479 KAKRERVVOEKRAVGMLGFLGGAACSTMGAITSVALTVQARQLLGGIVOCQNNLRA	538	Db	442 PPSGQIRCSSNTGSLITRDGCNNNGSEIIRPGGDMRNWSLSELYKVKTEBPLGV	501
Db	500 KAKRERVVOEKRAVG-TIGFLFLGFLGGAACSTMGAITSVALTVQARQLLGGIVOCQNNLRA	558	Qy	476 APTKAKRERVVOEKRAVGMLGAMFLGFLGGAACSTMGAITSVALTVQARQLLGGIVOCQNNL	535
Qy	539 IKAQOHLQCLTWTGKIKOLQARIALLAVERYLKDKOILLGFWGICSGKLUICTAVPNNASWNTK	598	Db	502 APTKAKRERVVOEKRAVG-IGFLFLGFLGGAACSTMGAITSVALTVQARQLLGGIVOCQNNL	560
Db	559 IEAQOHLQCLTWTGKIKOLQARIALLAVERYLKDKOILLGFWGICSGKLUICTAVPNNASWNTK	618	Qy	536 LRAIKAOQHLLQCLTWTGKIKOLQARIALLAVERYLKDKOILLGFWGICSGKLUICTAVPNNASW	595
Qy	599 LDQIWNNTWMWDRDIDNYTHLITYLTLIESQNEQKQNEQELQLDKMSL	649	Db	561 LRAIEAQHLLQCLTWTGKIKOLQARIALLAVERYLKDKOILLGFWGICSGKLUICTAVPNNASW	620
Db	619 LEQIWNNTWMWDRDIDNYTHLITYLTLIESQNEQKQNEQELQLDKMSL	669	Qy	596 NKTLDOIWNNTWMWDRDIDNYTHLITYLTLIESQNEQKQNEQELQLDKMSL	649
Db	621 NKSLEQIWNNTWMWDRDIDNYTHLITYLTLIESQNEQKQNEQELQLDKMSL	674	Db	621 NKSLEQIWNNTWMWDRDIDNYTHLITYLTLIESQNEQKQNEQELQLDKMSL	674
RESULT 14					
VCJLV env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)					
N Alternative names: coat polyprotein					
C:Species: human immunodeficiency virus type 1, HIV-1					
A:Host: Homo sapiens (man)					
C:Accession: A03975					
R:Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.					
Cell: 40, 9-17, 1985					
A:Title: Nucleotide sequence of the AIDS virus, LAV.					
A:Reference number: A90866; MUID:85099333; PMID:2981635					
A:Accession: A03975					
A:Molecule type: DNA					
A:Residues: 1-861 <WAT>					
A:Cross-references: UNIPROT:PO3377; UNIPARC:UPI000012A013; GB:K02013; NID:9326417; PIDN:					
C:Genetics:					
C:Superfamily: type E retrovirus env polyprotein					
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein					
P:1-30/Domain: signal sequence #status predicted <EXT>					
P:31-516/Product: transmembrane glycoprotein #status predicted <TM>					
P:517-861/Product: exterior membrane glycoprotein #status predicted <TM>					
P:881-1461/Protein: transmembrane glycoprotein #status predicted <TM>					
P:816, 621, 630, 642, 679, 755, 821/Binding site: carbohydrate (Asn) (covalent) #status predicted					
Q:3 LWTYYGVPWKEAATTLFCASDAKAYDTEAHHVATHACVPTNPNQEVVLENTENF					
Q:3 LWTYYGVPWKEAATTLFCASDAKAYDTEAHHVATHACVPTNPNQEVVLENTENF					
Q:63 NMWKNNNVYQMHEDIISMDQSLKPCVYLTKPLCYTLCNTDL-TN-NTNTTELTSIV					
Q:63 NMWKNNNVYQMHEDIISMDQSLKPCVYLTKPLCYTLCNTDL-TN-NTNTTELTSIV					
Q:94 NMWKNNNVYQMHEDIISMDQSLKPCVYLTKPLCYTLCNTDL-TN-NTNTTELTSIV					
Q:120 WEOQKGEMRNCSNNTISIRDKVQEVALFYKLUDEVDDNNNTNTKYLINCNTSV					
Q:120 WEOQKGEMRNCSNNTISIRDKVQEVALFYKLUDEVDDNNNTNTKYLINCNTSV					
Q:154 ME---KGEIKNCNFNISISRGVKEYAFFYKLDIPIDN----DTTSYLTLSCTNSV					
Q:180 ITQACPVYSFEPPIPHYCPTGFLALLKNDKFENGTCPTCNSTVQCTHIGRPVYSTQ					
Q:180 ITQACPVYSFEPPIPHYCPTGFLALLKNDKFENGTCPTCNSTVQCTHIGRPVYSTQ					
Q:240 LNSGLAAEEPVVISENFNTNAKTIQVNVSVEINCRPNNSTRK-RVTLGPGRVWYT					
Q:240 LNSGLAAEEPVVISENFNTNAKTIQVNVSVEINCRPNNSTRK-RVTLGPGRVWYT					
C:Query Match					
C:Best Local Similarity: 80.1%; Score: 2782; DB: 2; Length: 851;					
C:Best Local Similarity: 82.0%; Score: 80.4e-16; DB: 2; Length: 851;					
C:Matches 534; Conservative 39; Mismatches 54; Indels 24; Caps 9;					
C:Accession: S33985					
C:Carlini, F.					
C:Submitted to the EMBL Data Library, November 1991					
C:Reference number: S33979					
C:Accession: S33985					
C:Status: Preliminary					
C:Molecule type: mRNA					
C:Cross-references: UNIPROT:Q78243; UNIPARC:UPI00001067CD; EMBL:211530; PIDN:					
C:SuperFamily: type B retrovirus env polyprotein					
Q:Query Match					
Q:Best Local Similarity: 80.1%; Score: 2782; DB: 2; Length: 851;					
Q:Best Local Similarity: 82.0%; Score: 80.4e-16; DB: 2; Length: 851;					
Q:Matches 534; Conservative 39; Mismatches 54; Indels 24; Caps 9;					
Q:Accession: S33985					
Q:Carlini, F.					
Q:Submitted to the EMBL Data Library, November 1991					
Q:Reference number: S33979					
Q:Accession: S33985					
Q:Status: Preliminary					
Q:Molecule type: mRNA					
Q:Cross-references: UNIPROT:Q78243; UNIPARC:UPI00001067CD; EMBL:211530; PIDN:					
C:Genetics:					
C:Gene: env					
C:Superfamily: type E retrovirus env polyprotein					
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein					
P:1-30/Domain: signal sequence #status predicted <EXT>					
P:31-516/Product: exterior membrane glycoprotein #status predicted <TM>					
P:517-861/Product: transmembrane glycoprotein #status predicted <TM>					
P:881-1461/Protein: transmembrane glycoprotein #status predicted <TM>					
P:816, 621, 630, 642, 679, 755, 821/Binding site: carbohydrate (Asn) (covalent) #status predicted					
Q:3 LWTYYGVPWKEAATTLFCASDAKAYDTEAHHVATHACVPTNPNQEVVLENTENF					
Q:3 LWTYYGVPWKEAATTLFCASDAKAYDTEAHHVATHACVPTNPNQEVVLENTENF					
Q:63 NMWKNNNVYQMHEDIISMDQSLKPCVYLTKPLCYTLCNTDL-TN-NTNTTELTSIV					
Q:63 NMWKNNNVYQMHEDIISMDQSLKPCVYLTKPLCYTLCNTDL-TN-NTNTTELTSIV					
Q:94 NMWKNNNVYQMHEDIISMDQSLKPCVYLTKPLCYTLCNTDL-TN-NTNTTELTSIV					
Q:120 WEOQKGEMRNCSNNTISIRDKVQEVALFYKLUDEVDDNNNTNTKYLINCNTSV					
Q:120 WEOQKGEMRNCSNNTISIRDKVQEVALFYKLUDEVDDNNNTNTKYLINCNTSV					
Q:154 ME---KGEIKNCNFNISISRGVKEYAFFYKLDIPIDN----DTTSYLTLSCTNSV					
Q:180 ITQACPVYSFEPPIP HYCPTGFLALLKNDKFENGTCPTCNSTVQCTHIGRPVYSTQ					
Q:180 ITQACPVYSFEPPIP HYCPTGFLALLKNDKFENGTCPTCNSTVQCTHIGRPVYSTQ					
Q:240 LNSGLAAEEPVVISENFNTNAKTIQVNVSVEINCRPNNSTRK-RVTLGPGRVWYT					
Q:240 LNSGLAAEEPVVISENFNTNAKTIQVNVSVEINCRPNNSTRK-RVTLGPGRVWYT					
Q:264 FYNCSNTOFLNSAWNT SNGFTMSVTXQKDTGDFCPTCNSTVQCTHIGRPVYSTQ					
Q:301 LGNIROAHCNISRAQWNNTLQQIATTLREQFG-NKTIAPNQSSGGDPETVMSFNC					
Q:301 LGNIROAHCNISRAQWNNTLQQIATTLREQFG-NKTIAPNQSSGGDPETVMSFNC					
Q:324 -GMRQAHCNISRAKWNNTLKOIDSKLRFQFGNNTLQQIATTLREQFG-NKTIAPNQSSGGDPETVMSFNC					
Q:360 FYNCSNTOFLNSAWNT SNGFTMSVTXQKDTGDFCPTCNSTVQCTHIGRPVYSTQ					
Q:383 FYNCSNTOFLNSAWNT SNGFTMSVTXQKDTGDFCPTCNSTVQCTHIGRPVYSTQ					

Qy 419 KGLIRGSSNITGLLTRDGGGENOTTEIFRPGGDMRDWRSELYKKVIEPLGVAPT 478
Db 435 SGQIRCSSNITGLLTRDGGNSNNESRIFRPGGDMRDWRSELYKKVIEPLGVAPT 494

Qy 479 KAKRRVQREKRAVGMFLGFLGAAGSTMGATSMALTYQARQILSGTVOQONNLRA 538
Db 495 KAKRRVQREKRAVG-IGALETLGFLGAAGSTMGAASTMILTVQARQILSGTVOQONNLRA 553

Qy 539 IKAQHLLQIYTWGIKOLQARILAYERYLKDQQLGFWGSGKLICCTAVPNASWSNKT 598

Db 554 IEAQHLLQIYTWGIKOLQARILAYERYLKDQQLGFWGSGKPICTTAVPNASWSNKS 613

Qy 599 LDQINNMNTNEWDRBIDNTHLITLIESONQEQKNOELLQDKWASL 649

Db 614 LEQINNMNTNEWDRBINNTSLISLIESONQEQKNEQELLEDWKWASL 664

Search completed: March 7, 2006, 17:51:34
Job time : 51.7758 secs

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Scoring table:	BLOSUM62	
Searched:	2166443 seqs, 705528306 residues	
Total number of hits satisfying chosen parameters:	2166443	
Minimum DB seq length:	0	
Maximum DB seq length:	2000000000	
Post-processing:	Minimum Match 0% Maximum Match 100%	
Data bases:	UniProt 05.80: 1: uniprot_sprot: 2: uniprot_trembl: *	
Run on:	March 7, 2006, 17:40:55 ; Search time 297.698 Seconds (without alignments) 1538.097 Million cell updates/sec	
Title:	US-09-938-406-1_COPY_33_681	
Perfect score:	3474	
Sequence:	1 ANLWVTVYYGVPWVKATT.....QNQQEKNQQELQLDKWASL 649	
Scoring table:	Gapop 10.0 , Gapext 0.5	
ALIGNMENTS		
RESULT 1		
ID	ENV_HV1C4	STANDARD;
AC	P05879;	PRIT;
DT	01-NOV-1988 (Rel. 09, Created)	
DT	01-NOV-1988 (Rel. 09, Last sequence update)	
DT	13-SEP-2005 (Rel. 48, Last annotation update)	
DB	Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41).]	
DE	Name=ENV;	
GN	Human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1).	
OS	Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;	
OC	Lentivirus; Primate lentivirus group.	
OX	NCBI_TaxID=11687;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RX	MEDLINE-87041461; PubMed=3490666;	
RA	Dessai S.M., Kalayaraman V.S., Casey J.M., Srinivasan A., Andersen P.R., Devare S.G.;	
RA	"Molecular cloning and primary nucleotide sequence analysis of a distinct human immunodeficiency virus isolate reveal significant divergence in its genomic sequences".	
RT	Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384 (1986).	
RL	[2]	
RN	PROTEIN SEQUENCE OF 34-43.	
RX	MEDLINE-90255924; PubMed=2187500;	
RA	Dayico A.L., Copeland T., Oroszlan S., Gallo R.C., Sarnighadharan M.G.;	
RA	"Characterization of the secreted, native gp120 and gp160 of the human immunodeficiency virus type 1."	
RT	AIDS Res. Hum. Retroviruses 6:371-380 (1990).	
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.	
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.	
CC	EMBL; MI3137; AAA4311.1; -; Genomic_RNA.	
DR	C25523; VCLJH4.	
DR	HSSP; PI9549; IMEQ.	
DR	SMR; P05879; 84-128, 87-212, 206-503, 552-638.	
DR	HTV; MI3137; ENVS_CDC45.	
DR	InterPro; IPR000777; GP120.	
DR	Pfam; PF0516; GP120; 1.	
DR	Pfam; PF0511; GP11; 1.	
KW	AIDB; Capsid protein; Direct Protein sequencing; Glycoprotein;	
KW	Polyprotein; Signal; Structural protein; Transmembrane.	
FT	SIGNAL 1	33
FT	CHAIN 34	522
FT	CHAIN 523	868
FT	CARBOHYD 89	89
FT	CARBOHYD 131	131

FT	CARBOHYD	138	N-linked (GLENAC. .)	(Potential).	Db	453 LIRCSNITGLLTRDGGENOTTEIFRGDDMRDNWRSLEYKVKVIEPLGVAPTKA 512
FT	CARBOHYD	139	N-linked (GLENAC. .)	(Potential).	Db	481 KRRVYORKRRAVGMIGAMFLGFGAAGSTMATGATSMALTYQARQLLSGIVQQNNLRAIK 540
FT	CARBOHYD	142	N-linked (GLENAC. .)	(Potential).	Db	513 KRRVYORKRRAVGMIGAMFLGFGAAGSTMATGATSMALTYQARQLLSGIVQQNNLRAIK 572
FT	CARBOHYD	162	N-linked (GLENAC. .)	(Potential).	Qy	541 AQQHLQLTVWGIKOLQRILAVLERYLKQDQLLGFGCGSKLJCTAVPNASWSNKTLID 600
FT	CARBOHYD	166	N-linked (GLENAC. .)	(Potential).	Db	573 AQDQLQLTVWGIKOLQRILAVLERYLKQDQLLGFGCGSKLJCTAVPNASWSNKTLID 632
FT	CARBOHYD	195	N-linked (GLENAC. .)	(Potential).	Qy	601 QIWNNTMMEWDREIDNYTHLYTLLIESQNQEKQELQLDKWASL 649
FT	CARBOHYD	198	N-linked (GLENAC. .)	(Potential).	Db	633 QIWNNTMMEWDREIDNYTHLYTLLIESQNQEKQELQLDKWASL 681
FT	CARBOHYD	208	N-linked (GLENAC. .)	(Potential).		
FT	CARBOHYD	245	N-linked (GLENAC. .)	(Potential).		
FT	CARBOHYD	252	N-linked (GLENAC. .)	(Potential).		
FT	CARBOHYD	273	N-linked (GLENAC. .)	(Potential).		
FT	CARBOHYD	287	N-linked (GLENAC. .)	(Potential).		
FT	CARBOHYD	300	N-linked (GLENAC. .)	(Potential).		
FT	CARBOHYD	306	N-linked (GLENAC. .)	(Potential).		
FT	CARBOHYD	312	N-linked (GLENAC. .)	(Potential).		
FT	CARBOHYD	342	N-linked (GLENAC. .)	(Potential).		
FT	CARBOHYD	349	N-linked (GLENAC. .)	(Potential).		
FT	CARBOHYD	365	N-linked (GLENAC. .)	(Potential).		
FT	CARBOHYD	371	N-linked (GLENAC. .)	(Potential).		
FT	CARBOHYD	395	N-linked (GLENAC. .)	(Potential).		
FT	CARBOHYD	405	N-linked (GLENAC. .)	(Potential).		
FT	CARBOHYD	409	N-linked (GLENAC. .)	(Potential).		
FT	CARBOHYD	459	N-linked (GLENAC. .)	(Potential).		
FT	CARBOHYD	473	N-linked (GLENAC. .)	(Potential).		
FT	CARBOHYD	623	N-linked (GLENAC. .)	(Potential).		
FT	CARBOHYD	628	N-linked (GLENAC. .)	(Potential).		
FT	CARBOHYD	637	N-linked (GLENAC. .)	(Potential).		
FT	CARBOHYD	649	N-linked (GLENAC. .)	(Potential).		
FT	CARBOHYD	828	N-linked (GLENAC. .)	(Potential).		
FT	DISULFID	55	By similarity.			
FT	DISULFID	75	By similarity.			
FT	DISULFID	120	By similarity.			
FT	DISULFID	127	By similarity.			
FT	DISULFID	132	By similarity.			
FT	DISULFID	163	By similarity.			
FT	DISULFID	229	By similarity.			
FT	DISULFID	258	By similarity.			
FT	DISULFID	239	By similarity.			
FT	DISULFID	307	By similarity.			
FT	DISULFID	341	By similarity.			
FT	DISULFID	387	By similarity.			
FT	DISULFID	394	429 By similarity.			
SQ	SEQUENCE	868 AA:	98699 MW:	A11527C5226F0C8 CRC64:		
Qy	1. ANLWVTYYGVPVWEATTTLFCASDAKAYDTBAHNWATHACVPTNPNEOEVYLENTVE	100.0%	Score 3474; DB 1;	Length 868;	Query Match	84.3%; Score 2927; DB 2;
Qy	2. ANLWVTYYGVPVWEATTTLFCASDAKAYDTBAHNWATHACVPTNPNEOEVYLENTVE	100.0%	Pred. No. 1e-266;	Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity	85.5%; Pred. No. 2.8e-23;
Qy	3. ANLWVTYYGVPVWEATTTLFCASDAKAYDTBAHNWATHACVPTNPNEOEVYLENTVE	100.0%	Mismatches 649; Conservative	Matches 555; Conservative	Mismatches 33;保守性匹配	33; Mismatches 45; Indels 16; Gaps 7;
Db	33 ANLWVTYYGVPVWEATTTLFCASDAKAYDTBAHNWATHACVPTNPNEOEVYLENTVE	92				
Qy	61 NFNWKNNVNEQMEHDIIISLWDQSLKPCKLTPICVLTNCSTDINTNNNTNTTELSTIIVWW	60				
Db	93 NFNWKNNVNEQMEHDIIISLWDQSLKPCKLTPICVLTNCSTDINTNNNTNTTELSTIIVWW	120				
Db	93 NFNWKNNVNEQMEHDIIISLWDQSLKPCKLTPICVLTNCSTDINTNNNTNTTELSTIIVWW	152				
Qy	121 EQRKGEMRNCSFNITTSRDKYOREYALFYKLDVEPIDDNIKNTNTKYRLINCNTSVI	180				
Db	153 EQRKGEMRNCSFNITTSRDKYOREYALFYKLDVEPIDDNIKNTNTKYRLINCNTSVI	212				
Qy	181 TQACPKVSEFPIHYCPTGFAILKNDKFKNGTGPCTNVSTVQCTHGRPVNSTOLL	240				
Db	213 TQACPKVSEFPIHYCPTGFAILKNDKFKNGTGPCTNVSTVQCTHGRPVNSTOLL	272				
Qy	241 NGSLAAEEVIVSENFTNNAKTTIVQLQVNVSEINCRPNHTRKRTVLTGPRGVWYTGEI	300				
Db	273 NGSLAAEEVIVSENFTNNAKTTIVQLQVNVSEINCRPNHTRKRTVLTGPRGVWYTGEI	332				
Qy	301 LGNIRQAQNISRAQWNTLQLQIAATTREQGNKTIAPNQSSCGDPETVMSFNCGBFF	360				
Db	333 LGNIRQAQNISRAQWNTLQLQIAATTREQGNKTIAPNQSSCGDPETVMSFNCGBFF	392				
Qy	361 YCNSTQLPNFSAWNTSNGTWSVTRKQDGTIDILPCRKQI1NRWQVGRAMALPIKG	420				
Db	393 YCNSTQLPNFSAWNTSNGTWSVTRKQDGTIDILPCRKQI1NRWQVGRAMALPIKG	452				
Qy	421 LIRCSSNITGLLTRDGGCENOTTEIFRGDDMRDNWRSLEYKVKVIEPLGVAPTKA	480				

Db	264	SLAEEETVIRSDNETDNAKTIVQVNESVEINCTRPNNTNTRKSINTGPGRAFYATEIG 323	Qy	2	NLWVTTYYGYPVWKRAATTTLFCASIDAKAYDTEAHNVWATHACVPPNPQEVVLENVTEN 61
Qy	303	NIROAHCNISRAQWNNTLQQIATTLREQFG-NKTIAPNQSSGGDPBEIVMFSNCCEBFY 361	Db	32	NLWVTTYYGYPVWKRAATTTLFCASIDAKAYDTEAHNVWATHACVPPNPQEVVLENVTEN 91
Db	324	DIRQAHCNLSTRAKNDTLLQIVTKLREQFGNNKTTVFNQSSGGDPBEIVMFSNCCEBFY 383	Qy	62	FNMWKKONMVBMHEIDISLMQSLKPCVKLTPLCVTLNCNTDL-NMNTNTNTTELSSLIVVV 120
Qy	362	CNSTOLFNSAVVTSNNTGWSVTRKQDGTDLTLPCKIQLINRQVVGKAMYALPIKG 421	Db	92	FNMWKKONMVBMHEIDISLMQSLKPCVKLTPLCVTLNCNTDL-NMNTNTNTTELSSLIVVV 144
Db	384	CDSTQLENTWENDNN---IRGSNSTQENITLPCKIQLINMGGVGKAMYAPPRGQ 438	Qy	121	EORGEGEMRNCFSNNTTSISDKVQBYALPKLDPEIDONKNTNTKYLRLNTSVI 180
Qy	422	IRCSNTTGLLITRDG-GENOTTEIFRGCGDMRDNWRSELYKVKYKEPLGVAPTKA 480	Db	145	--GMREBTKNCFSNNTTSISDKVQDYALPYRDLVYPDN----DNTSRLINCNTSTI 197
Db	439	IRCSNTTGLLITRDGERDGNTTEIFRGCGDMRDNWRSELYKVKYKEPLGVAPTKA 498	Qy	181	TQACPXVSFEPPIPHCTPFGFALKCNDKFKTGTCPTCNVSTCVQTHGIRPVSTQLLL 240
Qy	481	KRRVQBEKRAVGMGLAMFLGFLGAAGSTMATSMALTYQAROLLSGIVQOQNLLRAIK 540	Db	198	TQACPXVSFEPPIPHCTPAGFAIKCNDKFKTGTCPKNVSTCVQTHGIRPVSTQLLL 257
Db	499	KRRVQBEKRAVGTIGAMFLGFLGAAGSTMGAASMALTYQAROLLSGIVQOQNLLRAIE 558	Qy	241	NGSLAAEEVYVIRSENFTNNAKTTIYVOLNVSBEINGTRPNNTTRKVTILGPGRVWYTGEI 300
Qy	541	AQQLLQLTWVGIKQLOARLAVERYLKDQOLLGFMGCSGRCLICITAVPNASWNKTLD 600	Db	258	NGSLAAEEVYVTRSSNFTDNARKNITVOLKESVETNTRPNNTTRKSIHGPGRAFTGDI 317
Db	559	AQQLLQLTWVGIKQLOARLAVERYLKDQOLLGFMGCSGRCLICITAVPNASWNKSLD 618	Qy	301	LGNIROAHCNISRAQWNNTLQIATLREORG-NETIAFNQSSGGDPETWHSFNCGGEF 359
Qy	601	QIWNNTMMEWREIDNTYTHLTYLIESSONQEQKNOELIQLDKWASL 649	Db	318	IGDIQAHCNISRTKWNNTLNQIATLKEQFGNNNTTIVQSGSDPETWHSFNCGGEF 377
Db	619	KIWNNTMMEWREIDNTYTNLYLIESSONQEQKNEQEELIQLDKWASL 667	Qy	360	FYCNSTOLFNSAWNTTSNGTWSVTRQKDGT-DITLPCRIKQIINRQVYVGKAMYALPI 418
			Db	378	FYCNSTOLFNSWTNT--NGTWNLTOSNGTEGNDTITLPCRIKQIINMWWQEVGKAMYALPI 435
			Qy	419	KGLIRCSSNITGLLTRDGG-GENOTTEIFRPGGDMRDNWRSELYKVKYKVIBPLGVAP 477
AC	040222_040222_9HIV1	PRELIMINARY; PRT; 854 AA.	Db	436	RGQIRCSSNITGLLTRDGGNNHNDTETPRGGDMRDNWRSELYKVKYKVIBPLGVAP 495
DT	01-JAN-1998 (T-TMBLrel. 05, Created)		Qy	478	TKAKRERVQBEKRAVGMFLGJGAACSTMGATISMALTVQAQQLSGIVQQQNLRL 537
DT	01-JAN-1998 (T-TMBLrel. 05, Last sequence update)		Db	496	TKAKRERVQBEKRAVGTIGAMPFLGJGAACSTMGASITLVQARLLLSSGIVQQQNLRL 555
DE	Env polyprotein.		Qy	538	AIKAOHLLQLTWVGIKQLOARLAVERYLKDQOLLGFMGCSGRCLICITAVPNASWSNK 597
GN	Name-env;		Db	556	AIEAQHLLQLTWVGIKQLOARLAVERYLKDQOLLGFMGCSGRCLICITAVPNASWSNK 615
OC	Human immunodeficiency virus 1.		Qy	598	TLDQIWNNTMMEWREIDNTYTHLTYLIESSONQEQKNOELIQLDKWASL 649
OC	Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;		Db	616	TLDMTWNNTMMEWREIDNTYGLTYLIESSONQEQKNEQEELIQLDKWASL 667
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=AD8;				
RC	STRAIN=AD8;				
DR	Theodore T.S., Englund G., Buckler-White A., Buckler C.B., Martin M.A., Peden K.W.; "Construction and characterization of a stable full-length macrophage-tropic HIV type 1 molecular clone that directs the production of high titters of progeny virions.", AIDS Res. Hum. Retroviruses, 12:191-194(1996). [2]				
RN	RT				
RT	"Construction and characterization of a stable full-length macrophage-tropic HIV type 1 molecular clone that directs the production of high titters of progeny virions.", AIDS Res. Hum. Retroviruses, 12:191-194(1996).				
RN	RT				
RP	NUCLEOTIDE SEQUENCE.				
RA	Theodore T.S., Englund G., Buckler-White A., Buckler C.B., Martin M.A., Peden K.W.C.; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.				
RA	EMBL; AF004394; AAB64170.1; -; Genomic_DNA.				
DR	HSSP; P04578; 1DDB.				
DR	SMR; Q40222; 143-489, 538-624.				
DR	GO; GO:0016021; C:integral membrane; IEA.				
DR	GO; GO:0019031; C:viral envelope; IEA.				
DR	GO; GO:0005198; F:structural molecule activity; IEA.				
DR	InterPro; IPR000777; GPI20.				
DR	Pfam; PF00516; GP120; 1.				
DR	Pfam; PF00517; GP41; 1.				
KW	AIDS; Polyprotein; Transmembrane.				
SQ	SEQUENCE 854 AA; 97291 MW; 06C45E69103C6C12 CRC64;				
Query Match	83.7%	Score 2908; DB-22; Length 854;			
Best Local Similarity	84.0%	Pred. No. 9.1e-22; Indels 20; Gaps 7;			
Matches	548;	Conservative 36; Mismatches 48;			

DR	InterPro; IPR000328; Env GP41.	RX	DOI=10.1128/JVI.77.11.6359-6366.2003;
DR	Pfam; PF00516; GP120.	RA	Robbins K.E., Lemey P., Pybus O.G., Jaffe H.W., Youngpairoj A.S.,
DR	Pfam; PF00517; GP41; 1.	RA	Brown T.M., Salenit M., Vandamme A.M., Kalish M.L.,
KW	AIDS; Envelope protein; Transmembrane.	RT	"U.S. Human immunodeficiency virus type 1 epidemic: date of origin, population history, and characterization of early strains.";
FT	NON_TER 1	RL	J. Virol. 77:6359-6366(2003).
SEQUENCE	853 AA; 96993 MW;	DR	EMBL; AY24718; ARP37146; 1; -; Genomic DNA.
SQ	7392EE340C50C4AD CRC64;	DR	HSSP; P20871; ICE4.
Query Match	83.7%; Score 2906.5; DB 2; Length 853;	DR	SMR; Q7SVL7; 1.95-4.96; 541-630.
Best Local Similarity	83.7%; Pred. No. 1.2e-221;	DR	GO; GO:0016021; C:integral membrane; IEA.
Matches	543; Conservative 46; Mismatches 47;	DR	GO; GO:0005198; C: viral envelope; IEA.
Db	3 LMWVYYGVPWKEATTTLFCASDAKAYTEAHNNWATHACVPTNPNPQEVLLENTEF 62	DR	InterPro; IPR00328; Env GP41.
Db	33 LMWVYYGVPWKEATTTLFCASDAKAYTEEVNNWATHACVPTDPPNPQEVLLENTEF 92	DR	IPR000777; GP120.
Qy	63 NMWNKNMVEQMHEDDISLWQDSLKPCVKLTCPLCYTLNCDLNTNTNTTELSIIVW 121	DR	Pfam; PF00516; GP120; 1.
Db	93 NMWNKNMVEQMHEDDISLWQDSLKPCVKLTCPLCYTLNCDL-DYRNATNTNS --- SWIK 146	DR	PF00517; GP41; 1.
Qy	3 LMWVYYGVPWKEATTTLFCASDAKAYTEAHNNWATHACVPTNPNPQEVLLENTEF 62	KW	AIDS; Envelope protein; Transmembrane.
Db	33 LMWVYYGVPWKEATTTLFCASDAKAYTEEVNNWATHACVPTDPPNPQEVLLENTEF 92	SEQUENCE	860 AA; 97762 MW; A7E1852 BD421590 CRC64;
Query Match	83.6%; Score 2905; DB 2; Length 860;	Best Local Similarity	84.2%; Score 2905; DB 2; Length 860;
Matches	548; Conservative 41; Mismatches 48;	Best Local Similarity	84.2%; Score 2905; DB 2; Length 860;
Db	33 LMWVYYGVPWKEATTTLFCASDAKAYTEEVNNWATHACVPTDPPNPQEVLLENTEF 92	Matches	548; Conservative 41; Mismatches 48; Indels 14; Gaps 7;
Qy	3 LMWVYYGVPWKEATTTLFCASDAKAYTEAHNNWATHACVPTNPNPQEVLLENTEF 62	Qy	3 LMWVYYGVPWKEATTTLFCASDAKAYTEAHNNWATHACVPTNPNPQEVLLENTEF 62
Db	33 LMWVYYGVPWKEATTTLFCASDAKAYTEEVNNWATHACVPTDPPNPQEVLLENTEF 92	Db	33 LMWVYYGVPWKEATTTLFCASDAKAYTEEVNNWATHACVPTDPPNPQEVLLENTEF 92
Qy	63 NMWNKNMVEQMHEDDISLWQDSLKPCVKLTCPLCYTLNCDLNTNTNTTELSIIVW 121	Qy	63 NMWNKNMVEQMHEDDISLWQDSLKPCVKLTCPLCYTLNCDLNTNTNTTELSIIVW 121
Db	93 NMWNKNMVEQMHEDDISLWQDSLKPCVKLTCPLCYTLNCDL-DYRNATNTNS --- SWIK 146	Db	93 NMWNKNMVEQMHEDDISLWQDSLKPCVKLTCPLCYTLNCDL-DYRNATNTNS --- SWIK 146
Qy	122 QRKGEMRNCFSNITTSIRDKVOREYALFYKLDVBPIDDNKNTNTNTKYRLNCNTSYLT 181	Qy	123 RGKCEMRNCFSNITTSIRDKVOREYALFYKLDVBPIDDNKNTNTNTKYRLNCNTSYLT 182
Db	147 PMERGBIKNGCSFNITTSIRDKVOREYALFYKLDVBPID---NDSENNTNTRLISNTSYLT 203	Db	147 MEKGIEKNGCSFNITTSIRDKVOREYALFYKLDVBPID---NDSENNTNTRLISNTSYLT 203
Qy	182 QACPVKSFEPPIPHCTPTGFAALKCNDKKEENGNGCPTCTVSTYQCTHGRPVYSTQTLIN 241	Qy	183 ACPKVSFEPPIPHCTPTGFAALKCNDKKEENGNGCPTCTVSTYQCTHGRPVYSTQTLIN 242
Db	204 QACPVKSFEPPIPHCTPTGFAALKCNDKKEENGNGCPTCTVSTYQCTHGRPVYSTQTLIN 263	Db	204 ACPKVSFEPPIPHCTPTGFAALKCNDKKEENGNGCPTCTVSTYQCTHGRPVYSTQTLIN 263
Qy	242 GSLABBEVIVSENFTNNAKTTIVOLANVSVEINCRPNHTRKVTLGGRVWYTTGEL 301	Qy	243 SIAAEVIVSENFTNNAKTTIVOLANVSVEINCRPNHTRKVTLGGRVWYTTGEL 302
Db	264 GDIROAHNCNTRSAWNNTNTRQIVELKGEFGNNKTIVFHSSGDPETVWHSFNCGGEF 383	Db	264 SIAAEVIVSENFTNNAKTTIVOLANVSVEINCRPNHTRKVTLGGRVWYTTGEL 323
Qy	302 GNIROAHNCNTRSAWNNTNTRQIATTLREOFGL-NCTTAPOSSGGDPETVWHSFNCGGEF 360	Qy	303 NIROAHNCNTRSAWNNTNTRQIATTLREOFGNKTTIAFNSGSDPEIYMHSEFNCGEFFYC 362
Db	324 GDIROAHNCNTRSAWNNTNTRQIVELKGEFGNNKTIVFHSSGDPETVWHSFNCGGEF 383	Db	324 DIQAHCNLSRTKWNTRQIVKLEROFGNKTTIAFNSGSDPEIYMHSEFNCGEFFYC 383
Qy	361 YCNSTOLPENSAWNNTSNGTWSUTRKQDKDGTITLPCRKTQIINRWWQVGKAMYALPIK 420	Qy	363 NSTOLFENSAWN--VTSNGTW-SVTRKQDKDGTITLPCRKTQIINRWWQVGKAMYALPIK 419
Db	384 YCNSTKLNFNT-TWNNTWNNTNSRDEEEITLPCRKTQIINRWWQVGKAMYALPIK 422	Db	384 DSTOLFENSTWNNTDTLFNSTWNNTDKGSNTTEDITLPCRKTQIINRWWQVGKAMYALPIK 443
Qy	421 LIRCSSNTGULLTRDGGENQTEIFRGCGMDNRWNESELYKKVYIEPLGVAPTKA 480	Qy	420 GLRCSSENITGULLTRDG-GENOTTEIFRGCGMDRDNRWNESELYKKVYIEPLGVAPTK 478
Db	443 QIRCSSNTGULLTRDGNDTSGIEIFRGCGMDNRWNESELYKKVYIEPLGVAPTKA 502	Db	444 GQIRCSSNTGULLTRDGNNKSETTEIFRGCGMDRDNRWNESELYKKVYIEPLGVAPTK 503
Qy	481 KRRVVQREGRAVGMFLGAMFLGFLGAAGSTMGATSMALTYQARQLLSGIVOOONNLRAK 540	Qy	479 KAKRRVREGRAVGMFLGAMFLGFLGAAGSTMGATSMALTYQARQLLSGIVOOONNLRAK 538
Db	503 KRRVVQREGRAVG-IGAMFLGFLGAAGSTMGAASTVLTLQARLLSGIVOOONNLRAK 561	Db	504 KAKRVRREGRAVGMFLGAMFLGFLGAAGSTMGATSMALTYQARQLLSGIVOOONNLRA 562
Qy	541 AQHQHQLQWTGKIQOLQARLTLAVERYLKDQQLGFWGCGSKLICLTAVPNASWNKTL D 600	Qy	539 IKAQQHQLQWTGKIQOLQARLTLAVERYLKDQQLGFWGCGSKLICLTAVPNASWNKMT 598
Db	562 AQHQHQLQWTGKIQOLQARLTLAVERYLKDQQLGFWGCGSKLICLTAVPNASWNKTL D 621	Db	563 IEAQQHQLQWTGKIQOLQARLTLAVERYLKDQQLGFWGCGSKLICLTAVPNASWNKS 622
Qy	601 QIWNMNTNEWDREIDNTYTHLITLLEBQNQEKNOQELLDKWASL 649	Qy	599 LDQIWNMNTNEWDREIDNTYTHLITLLEBQNQEKNOQELLDKWASL 649
Db	622 EIWNMNTNEWEKEIDNTYTNLIVNLEBQNQEKNOQELLDKWASL 670	Db	623 LDKIWNMNTNEWEKEIDNTYTNLIVNLEBQNQEKNOQELLDKWASL 673
RESULT	5	RESULT	6
Q7SVL7	SHIV1 PRELIMINARY;	Q7SVL7	Q6IVPO_9HIV1
ID		ID	Q6IVPO_9HIV1 PRELIMINARY;
AC		AC	Q6IVPO_9HIV1 PRELIMINARY;
DT	01-OCT-2003 (TREMBrel. 25, Created)	DT	05-JUL-2004 (TREMBrel. 26, Last annotation update)
DT	01-OCT-2003 (TREMBrel. 25, Last sequence update)	DE	Envelope glycoprotein.
GN	Name=env;	GN	Name=env;
OS	Human immunodeficiency virus 1.	OS	Human immunodeficiency virus 1.
OC	Lentivirus; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;	OC	Lentivirus; Primate lentivirus group.
OX		OX	
NCBI_TaxID	11676;	NCBI_TaxID	11676;
RP	NUCLEOTIDE_SEQUENCE;	RP	MEDLINE=22628496; PubMed=12743293;
RX		RX	

RESULT 6
Q6IVPO_9HIV1
ID Q6IVPO_9HIV1 PRELIMINARY;
AC Q6IVPO_9HIV1 PRELIMINARY;
DT 05-JUL-2004 (TREMBrel. 27, Created)

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)	Db 572 RAIKEQQHLLQLTYWIKIQKOLQARYLAVERYLDRDQQLLGWCGSGKLIICHTAVPNASWN 631
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)	Qy 597 KTLDDIWNNTWMEWDREDNYTHIYTIBESONQEQRNQELLIQDKWASL 649
DE Envelope glycoprotein (Fragment).	Db 632 KSMDEIWNNTWMEWEIDNYTGLYLNLEKSONQERNEQELIALLDKWANL 684
GN Human immunodeficiency virus 1.	
OS Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;	
OC Lentiviruses; Primate lentivirus group.	
NCBI TaxID:11676;	
RN [1]	
RP NUCLEOTIDE SEQUENCE.	
PubMed:14390699; DOI:10.1128/JVI.78.6.2790-2807.2004;	RX Q7SVL5_9HIV1 PRELIMINARY; PRM; 852 AA.
RX PubMed:14390699; DOI:10.1128/JVI.78.6.2790-2807.2004;	AC Q7SVL5_;
RA Kuhmann S. B., Pugach P., Kunstman K. J., Taylor J., Stanfield R. L., Snyder A. A., Strizik J. M., Riley B. T., Baroudy B. M., Wilson I. A., Korber B. T., Wolinsky S. M., Moore J. P.; "Genetic and phenotypic analyses of human immunodeficiency virus type 1 escape from a small-molecule CCR5 inhibitor.";	DT 01-OCT-2003 (TREMBLrel. 25, Created)
DR EMBL:AY357551; AAR00905.1; -; Genomic_DNA.	DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DR HSSP; P04578; IK33.	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DR SMR; Q6UYO0; 93-147; 209-507; 552-641.	DB Envelope glycoprotein.
DR GO:0016021; C:integral to membrane; IEA.	GN Name=env;
DR GO:0019301; C:viral envelope; IEA.	OS Human immunodeficiency virus 1.
DR GO:0005198; F:structural molecule activity; IEA.	OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
DR InterPro; IPR000328; Env GP41.	OC Lentivirus; Primate lentivirus group.
DR InterPro; IPR000777; GP20.	OX NCBI_TaxID:11676;
DR Pfam; PF00516; GP120; 1.	RN
DR Pfam; PF00517; GP41; 1.	RP NUCLEOTIDE SEQUENCES.
DR AIDS; Envelope protein; Transmembrane.	RX MEDLINE:22628496; PubMed:12743293;
FT NON_TER 1 AA; 98144 MW; 02DB82C72985648EC CRC64;	RX DOI:10.1128/JVI.77.11.6359-6366.2003;
SQ SEQUENCE 863 AA; 98144 MW; 02DB82C72985648EC CRC64;	RA Robbins K. E., Lemey P., Pybus O. G., Jaffe H. W., Youngjaeiroj A.S., Brown T. M., Salemi M., Vandamme A. M., Kalish M.L.; "U.S. Human immunodeficiency virus type 1 epidemic: date of origin, population history, and characterization of early strains.";
Query Match 83.5%; Score 2900.5%; DB 2; Length 863; Best Local Similarity 83.5%; Pred. No. 3.6e-221; Mismatches 45; Conservative 50; Indels 13; Gaps 8; Matches 545; Conservation 45; Mismatches 50; Indels 13; Gaps 8;	RT "J. Virol. 77:6359-6366 (2003)."
Db 2 NLWVTTYYGVPWKMEVNQHEIDLSLWQSLKPCVKLPLCYLNLCDLN-TNNNTTELSIIVWW 120	RT DRBML; AV247222; AAP37148.1; -; Genomic_DNA.
Db 100 FNMWQNMMVEQMHEDLSLWQSLKPCVKLPLCYLNLCDLN-TNNNTTELSIINATNS----SW 154	RT RLM; P04578; 1DLB.
Qy 2 NLWVTTYYGVPWKMEVNQHEIDLSLWQSLKPCVKLPLCYLNLCDLN-TNNNTTELSIIVWW 120	RT DR SMR; P04578; 1DLB.
Db 40 NLWVTTYYGVPWKMEVNQHEIDLSLWQSLKPCVKLPLCYLNLCDLN-TNNNTTELSIIVWW 120	RT DR GO:0016021; C:integral to membrane; IEA.
Qy 62 FNMWQNMMVEQMHEDLSLWQSLKPCVKLPLCYLNLCDLN-TNNNTTELSIIVWW 120	RT DR GO:0005198; C:viral envelope; IEA.
Db 100 FNMWQNMMVEQMHEDLSLWQSLKPCVKLPLCYLNLCDLN-TNNNTTELSIIVWW 120	RT DR InterPro; IPR000328; Env GP41.
Qy 121 -EQRGKGMENCSFNITTSIRDKVQEYALFYKLDYVEPTIDDKNNTNNKYRLINCNTS 179	RT DR InterPro; IPR000777; GP20.
Db 155 GBPMEGEIIKNCFSFNITTSIRDKVQEYALFYKLDYVEPTIDDKNNTNNKYRLINCNTS 214	RT DR Pfam; PRO0516; GP120; 1.
Qy 180 ITQACPVKSPFPIPHYCTPGPALKNDKKFNGTGPCTNVSTQCTGIRPVSTQI 239	RT DR SEQ: Q7SVL5 AA; 96680 MW; F8D811028025D998 CRC64;
Db 215 ITQACPVKSPFPIPHYCAPGFLALKNDKKFNGTGPCTNVSTQCTGIRPVSTQI 274	RT DR SEQUENCE 863 AA; 96680 MW; F8D811028025D998 CRC64;
Qy 240 LNGSLAAEVIRSENFTNNAKTTIVQLNVSVEINTPRNNHTRCRVTLGPGRWYTTG 299	Query Match 83.4%; Score 2899; DB 2; Length 852;
Db 275 LNGSLAAEVIRSENFTNNAKTTIVQLNVSVEINTPRNNHTRCRVTLGPGRWYTTG 334	Best Local Similarity 83.9%; Pred. No. 4.7e-221;
Qy 300 ILGNTRIOAHCNISRAQWNTLQQTATTLREFQFG-NKTTIAFNQSSGGDPETVMHSFNCGSE 358	Matches 546; Conservative 36; Mismatches 47; Indels 22; Gaps 6;
Db 335 IIGDIRKAHCNISRAQWNTLKHIVEKLKGFOFGNNTTIVFHSSGGDPETVMHSFNCGSE 394	Qy 3 LWWVTTYYGVPWKMEVNQHEIDLSLWQSLKPCVKLPLCYLNLCDLN-TNNNTTELSIIVWW 120
Qy 359 FFYCNCSTQLENSAWNNTSGTW--SYTRKQDGTGDLITLPCRQIOLINRQVICKAMYL 416	Db 33 LWWVTTYYGVPWKMEVNQHEIDLSLWQSLKPCVKLPLCYLNLCDLN-TNNNTTELSIIVWW 120
Db 395 FFYCNCSTKLFNSTW-TWNNGTWTTRANTERSNSTEEKITLPCCRQIOTINNMQEVCKAMYP 453	Qy 33 LWWVTTYYGVPWKMEVNQHEIDLSLWQSLKPCVKLPLCYLNLCDLN-TNNNTTELSIIVWW 120
Qy 417 PIKGLRCSSNITGLLTDGGENOTIEFRPGGGDMRDNWRSSELYKVKVKEPLGTA 476	Db 34 LWWVTTYYGVPWKMEVNQHEIDLSLWQSLKPCVKLPLCYLNLCDLN-TNNNTTELSIIVWW 120
Db 454 PIRGKRCSSNITGLLTD-GGTNTNTETRGPGGGDMRDNWRSSELYKVKVRLBPLGTA 512	Qy 35 LWWVTTYYGVPWKMEVNQHEIDLSLWQSLKPCVKLPLCYLNLCDLN-TNNNTTELSIIVWW 120
Qy 477 PTKAKRVRVOREKRAVGMGLAMEFLGLAAGSTMGATSMALTYQARQILSGIVQQNNL 536	Db 36 LWWVTTYYGVPWKMEVNQHEIDLSLWQSLKPCVKLPLCYLNLCDLN-TNNNTTELSIIVWW 120
Db 513 PTEAKRVRVOREKRAVY-IGAVLGLFLGAAGSTMGAESTLTVQRQLISGIYQQNNL 571	Qy 37 LWWVTTYYGVPWKMEVNQHEIDLSLWQSLKPCVKLPLCYLNLCDLN-TNNNTTELSIIVWW 120
Qy 537 RAIKAQOHLLQLTWGIKOLQARIЛАVERYLKDQQLGWFGSGKLICLTAVPNASWN 596	Db 38 LWWVTTYYGVPWKMEVNQHEIDLSLWQSLKPCVKLPLCYLNLCDLN-TNNNTTELSIIVWW 120

Qy	419 KGLIRCSSNITGLLITRGGGENOTTEIIPPGGDMRDWRSELKYKVKIEPLGVAPT	478	Qy	233 VVSTOLLINGSLAEEVVIRSENFTNNNAKTTIVQLANVSVEINCTRPNNHTRKRVTLGPR 292	
Db	436 RGQTICRSSNITGLLITRGGSNENTDEIIPPGGMMRDWRSELKYKVKIEPLGVAPT	495	Db	275 VVSTOLLINGSLAEEEVIRSENFTNNNAKTTIVQLANVSVEINCTRPNNHTRKRVTLGPR 334	
Qy	479 KAKRVRVQREKRAVGMFLGAASTMGATSMALTVQARQLLSGIVQQONLLRA 538		Qy	293 VVTTGEILGNTIROAHCNISRAQNTTQLQIATTLEQFGNKTAFNQSSGDPETVYHNS 352	
Db	496 KAKRVRVQREKRAVGMFLGAASTMGATSMALTVQARQLLSGIVQQONLLRA 554		Db	335 VTTGEIVGDIRKAHCNISRTONTLKHIVEKLQPKQFNGNNTTFNHSQSGDPETVYHNS 394	
Qy	539 1KAQHLLQTLTWGKQLQARLAVERYLKDQOLIGFNGCSKLICLTAVPNAWSNKT 598		Qy	353 FNGCGEFFYCNSNOSTOLENSAWNTISNGTSVTRKQDPSDITLPLCRIKQIINNWQVCKA 412	
Db	555 1EAQHLLQTLTWGKQLQARLAMERYLKDQOLIGFNGCSKLICLTAVPNAWSNKS 614		Db	395 FNGCGEFFYCNSTKLFENSTW-TENNNTWT-TERNSTSTEHTLPLCRIQINNWQEVCKA 452	
Qy	599 LDQITANMTMWEIDNTHLYLIVBESQNQEKNQELLOLDKWAHL 649		Qy	413 MYALPKIGLIRCSNNITGLLITRGG-GENOTBEFRGGDMRDWRSELKYKVKIB 471	
Db	615 LDNTWNNTMWEIDNTHLYLIVBESQNQEKNQELLOLDKWAHL 665		Db	453 VYAPPTRKIRCNSNNITGLLITRGGNDTRGEBIFRGGGDMRDWRSELKYKVKIB 512	
<hr/>					
RESULT 8					
Q6IYM7	Q6IYM7 9HIV1 PRELIMINARY;	PRT;	869 AA.	Qy	472 PLGVAPTKAKRYYQREKRAVGMFLGAAGSTMGATSMALTYQAROLLSGIVQQ 531
ID	Q6IYM7;			Db	513 PLGIATPEAKRYYQREKRAVGLGAMFLGFGAAGSTMGAASVALTVQAROLLSGIVQQ 572
DT	05-JUL-2004 (TREMBrel. 27, Created)			Qy	532 QNNILRAIAKQOHLQTLTWGKQLQARLAVERYLKDQOLIGFNGCSKLICLTAVPWN 591
DT	05-JUL-2004 (TREMBrel. 27, Last sequence update)			Db	573 QNNILRAIAQOHLQTLTWGKQLQARLAVERYLKDQOLIGFNGCSKLICLTAVPWN 632
DE	Envelope glycoprotein (Fragment)			Qy	592 ASWSNKTELDQWINNTMWEIDNTHLYLIVBESQNQEKNQELLOLDKWAHL 649
GN	Name=env;			Db	633 ASWSNRSDIDEINNTMWEIDNTHLYLIVBESQNQEKNQELLOLDKWAHL 690
OS	Human immunodeficiency virus 1.				
OC	Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;				
NCBI_TaxID	Primate lentivirus group.				
OX	NCBI_TaxID=11676;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RX	PubMed=14990639; DOI=10.1128/JVI.78.6.2790-2807.2004;				
RA	Kuhmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L., Snyder A., Strizki J.M., Baroudy B.M., Wilson I.A., Korber B.T., Wollinsky S.M., Moore J.P.; "Genetic and phenotypic analyses of human immunodeficiency virus type 1 escape from a small-molecule CCR5 inhibitor"; J. Virol. 78:2790-2807 (2004).				
DR	GO:0019031; C: integral to membrane; IEA.				
DR	GO:0005198; C: viral envelope; IEA.				
DR	EMBL; AR357566; AR0918.1; -; Genomic_DNA.				
DR	GO:0016021; C:integral to membrane; IEA.				
DR	InterPro: IPRO000388; Env GP41.				
DR	InterPro: IPRO00777; GP120.				
DR	Pfam: PF00516; GP20; 1.				
DR	Pfam: PF00517; GP41; 1.				
DR	AIDS ; Envelope protein; Transmembrane.				
FT	NON_TER 1 1				
SQ	SEQUENCE 869 AA; 99123 MW; FE2BE1E50EFICC9A CRC64;				
Query Match Score 2898.5; DB 2; Length 869;					
Best Local Similarity 83.4%; Pred. No. 5.3e-221;					
Matches 543; Conservative 48; Mismatches 50; Indels 17; Gaps 8;					
Qy	2 NLWVTYYGVPVWKVEATTLFCASDAKAYDTAEHWVWATHACVPTNPNQEVVLTEN 61			Query Match Score 2896.5; DB 2; Length 853;	
Db	40 NLWVTYYGVPVWKVEATTLFCASDAKAYDTAEHWVWATHACVPTNPNQEVVLTEN 99			Best Local Similarity 83.6%; Pred. No. 7.4e-221;	
Qy	62 FNMKQNNMVEQHEDIIISWQSLKPCVKTLPCLVNTCTDL--NTNNNTTNTLISIV 118			Matches 544; Conservative 40; Mismatches 48; Indels 19; Caps 6;	
Db	100 FNMKQNNMVEQHEDIIISWQSLKPCVKTLPCLVNTCTDLVKNATNTN---- 154			Qy 2 NLWVTYYGVPVWKVEATTLFCASDAKAYDTAEHWVWATHACVPTNPNQEVVLTEN 61	
Qy	119 VW-BQRGKGEMRNCFSNNTSIRDKVQBYALFYKLDVPIIDD--NKNTNN--TKYR 172			Db 32 NLWVTYYGVPVWKVEATTLFCASDAKAYDTAEHWVWATHACVPTNPNQEVVLTEN 91	
Db	155 SWGPMPERGEIKNCFSNNTSIRDKVQBYALFYKLDVPIIDNSNNDDNNNNNTYRL 214			Qy 62 FNMKQNNMVEQHEDIIISLWDQSLKPCVKTLPCLVNTCTDL-NNTNTNTTELS:IVWW 120	
Qy	173 INCNTSVTQAQPKVSFEPITPHCTPFGALKCNDKFKENGTPGCTNVSTVQCTHGRP 232			Db 215 ISCTNSVITQAQPKVSFEPITPHCAPAGFAILRKCNDRKFFGTCPTNVSTVQCTHGRP 274	
Db	92 FNMKQNNMVEQHEDIIISLWDQSLKPCVKTLPCLVNTCTDLRNTNNNSSE----- 144				

Qy	121 EQRKGKEMRNCFSNITTSIRDVKOREYALFYKLDVPIIDNNKNTNTKYRLINCNTSYT 180	Query Match 83.4%; Score 2896.5; DB 2; Length 863;
Db	145 --GMREBIRNSFNITTSIRDVKDYLQYRLDVPII-----DNTSTRINCNTSYI 197	Best Local Similarity 82.9%; Pred. No. 7.6e-221; Mismatches 48; Indels 19; Gaps 8;
Qy	181 TOACPXSFEPPIHYCTPGFALKCNDFKENGSTGPCTNVSYTQCTHGIRPVYSTOILL 240	Matches 544; Conservative 45; Gaps 8;
Db	198 TOACPXSFEPPIHYCTPGFALKCNDFKENGSTGPCTNVSYTQCTHGIRPVYSTOILL 257	Qy 2 NLWVTVYGPWVKATTTLFCASDAKAYDTDEAHNVWATHACVPTNPQEVVLEVNTE 61
Qy	241 NGSLABEVTIRSENFTNATKIIYQLNVSVEINCTRPNHTRGVTLGGRWVTTGEI 300	Db 40 NLWVTVYGPWVKATTTLFCASDAKAYDTDEAHNVWATHACVPTDPNQEVVLEVNTE 99
Db	258 NGSLABEVTIRSSNFTDIAKNIYQLKSEVEINCTRPNNTRSIHGICPGRAYTTGEI 317	Qy 62 FMMKKNMVEQMHEIIISLWDQSLPKPCVLTPLCIVLNCTDLN-TNNFTNTTELISIIVWW 120
Qy	301 LGNIROAHCNISRAOWNNTLQIAITLREQFG-NKTIAPNQSSGDPETVMHSFNCGGF 359	Db 100 FMMKKNMVEQMHEIIISLWDQSLPKPCVLTPLCIVLNCTDKNTNNATSTNS---SW 154
Db	318 IGDIROAHCNISRTKWNNTINQIAITKLKEOFGNKNTIVFQSSGDPETVMHSFNCGGF 377	Qy 121 -EQRGKEMRNCFSNITTSIRDVKYQREVALFYKLDVEPIDDNNKNTNTKYRLINCNTSY 179
Qy	360 FYCNSTOLENSAWNNTSNGTMWSVTRKQDG-DIILPCKIQIINRQYVGKAMYALPI 418	Db 155 GEPMRGEIKNCSPNITTSIRDVKQYQALFYKLDVPPIDNSNNTNTNYRLJSCNTSV 214
Db	378 FYCNSTOLENFNSTWNP--NGTWNLQSNGTECNDTITLPCKIQIINRQYVGKAMYAPP 435	Qy 180 ITQACPXSFEPPIHYCPTGPAFKCNDFKENGSTGPCTNVSYTQCTHGIRPVYSTOILL 239
Qy	419 KGLIQQSSNTGLLTRDGGENQTFIIFRPGGDMRDWRSLEYTKVTKVIEPLGVAPT 478	Db 215 ITQACPXSFEPPIHYCAGPAFKCNDFKENGIGPCTNVSYTQCTHGIRPVYSTOILL 274
Db	436 RQQIIRCSSNTGLLTRDGGTNTSSGSEIFRPGGDMRDWRSLEYTKVVKIEPLGVAPT 495	Qy 240 LNGSLAEEVVIRSNINFNNAKTIVQLNVSVEINCTRNHTRKRVTLJPGRYWTGEG 299
Qy	479 KAKRVRVQREKRAVGMFLGFLGAAGSTMGMATSMALTYQAROLLSGYQONNLJRA 538	Db 275 LNGSLAEEVVIRSNINFNNAKTIVQLNVSVEINCTRPNNTTRKRIISMGCPGVLYTGE 334
Db	496 KAKRVRVQREKRAVETGIANFLGFLGAAGSTMGMALTSITIVQARIJLSGYQONNLJA 555	Qy 300 ILGNTROAHCNISRAOWNNTLQIAITLREQFG-NKTIAPNQSSGDPETVMHSFNCGG 358
Qy	539 IKAQPHLQLLTWIKQLOQARILAYERVILKDQOLLGPGGSGKLICITTAVPMNASWNT 598	Db 335 IIGDIDRKAHNNTISIAQWNNTLKH1VETKLQKFQFNNTKTAFHNSGGDPPELMHSFNCGG 394
Db	556 TEAQPHLQLLTWIKQLOQARILAYERVILKDQOLLGPGGSGKLICITTAVPMNASWNT 615	Qy 359 FFYCNTSTOLENSAWNNTSNGTMWSVTRKQDKT---GDLITLPRKIQIINRQYVGKAM 413
Qy	* 599 LDQIWNNTMWEDIEINTHTLITYLIESONQEQKNDLQDQKWL 649	Db 395 FFYCNTSTKLFNSTW-TRDNFTWT---RNDETEGSNTTLEILPRKIQIINRQYVGKAM 449
Db	616 LDDMINDNNTMNEWERIEINTHTLITYLIESONQEQKNEQDLLADKWL 666	Qy 414 YALPKGLIRCSSNTGLLTRDGGGENOTETFRPGGDMRDWRSLEYTKVTRIEPL 473
Qy		Db 450 YAPPGRKICRCSNTGLLTRDGGNDTSRIEIPRGGDMRDWRSLEYTKVTRIEPL 509
Qy		Qy 474 GVAPTKAKERVVRKRAVGMFLGFLGAAGSTMGMATSMALTYQAROLLSGYQONN 533
Db		Db 510 GIAPPKAKERVVRKRAVGMFLGFLGAAGSTMGMATSMALTYQAROLLSGYQONN 568
Qy		Qy 534 NLIRAIKAQHLLQIYTNGIKOLQARILAYERVILKDQOLLGPGGSGKLICITTAVPMNAS 593
Db		Db 569 NLIRAIQAQHLLQIYTNGIKOLQARILAYERVILKDQOLLGPGGSGKLICITTAVPMNAS 628
Qy		Qy 594 WSNKTLQDQWNNTMWEDIEINTHTLITYLIESONQEQKNDLQDQKWL 649
Db		Db 629 WSNKSMDEIWNNTMWEMWEKEIDNTGLIYNLLESQNQERNEQELLADKWL 684
RESULT 10		
Q6UTN7 9HIV1	Q6UTN7 9HIV1 PRELIMINARY; PRT; 863 AA.	RESULT 11
ID	Q7SVL4_9HIV1 PRELIMINARY;	Q7SVL4_9HIV1
AC	Q7SVL4_9HIV1 PRELIMINARY;	ID
DT	05-JUL-2004 (TREMBrel. 27, Created)	Q7SVL4_9HIV1 PRELIMINARY;
DT	05-JUL-2004 (TREMBrel. 27, Last sequence update)	AC
DT	05-JUL-2004 (TREMBrel. 27, Last annotation update)	Q7SVL4_9HIV1 PRELIMINARY;
DB	Envelope glycoprotein (fragment).	DT
GN	Name=env;	DT
OS	Human immunodeficiency virus 1.	DE
OC	Lentiviruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;	DE
NCBI_TaxID	Primate lentivirus group.	DE
OX	NCBI_TaxID=11676;	DE
RN	NUCLEOTIDE SEQUENCE.	DE
RP	PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;	DE
RX	Kuhmann S. P., Pugach P., Kinsman K.R., Taylor J., Stanfield R.L., Snyder A., Strizik J.M., Riley J., Baroudy B.M., Wilson I.A., Korber B.T., Wolinsky S.M., Moore J.P.; "Genetic and phenotypic analyses of human immunodeficiency virus type 1 escape from a small-molecule CCR5 inhibitor.", J. Virol. 78:2790-2807 (2004).	DE
RA	InterPro: IPR000328; EnVP41.	DE
RA	PFam: PF00516; GP120; 1.	DE
DR	AIDS; Envelope protein; Transmembrane.	DE
DR	NON_TER 1 1 MW; DE3D7F76BF7BE4E5C CRC64;	DE
SQ	SEQUENCE 863 AA; 98318 MW;	DE

DR	HSSP; P20871; 1CE4.	OX	NCBI_TaxID=11676;
DR	SMR; Q7SVL4; 195-406, 534-620.	RN	NUCLEOTIDE SEQUENCE.
DR	GO; GO:0016021; C:integral to membrane; IEA.	RP	MEDLINE:22533916; PubMed=12646921; DOI=10.1038/nature01470;
DR	GO; GO:0019031; C:viral envelope; IEA.	RX	Wei X., Decker J.M., Wang S., Hui H., Kappes J.C., Wu X., RA
DR	GO; GO:0005198; F:structural molecule activity; IEA.	RA	Salazar-Gonzalez J.F., Salazar M.G., Kilby J.M., Saag M.S., RA
DR	InterPro; IPR000328; Env GP41.	RA	Konarova N.L., Nowak M.A., Hahn B.H., Kwong P.D., Shaw G.M.;
DR	InterPro; IPR000777; GPI20.	RT	"Antibody neutralization and escape by HIV-1."
PFam; PF00516; GP120; 1.	RL	Nature 422:307-312(2003).	
PFam; PF00517; GP41; 1.	DR	EMBL; AY23724; AAP57324.1; -; Genomic_RNA.	
KW	AIDS; Envelope protein; Transmembrane	DR	HSSP; P04578; 1D1B.
SEQUENCE 850 AA; 9653 MW;	DR	SNR; OTSUVA4; 545-631.	
SEQUENCE 850 AA;	DR	GO; GO:0016021; C:integral to membrane; IEA.	
Best Local Similarity 84.9%; Pred. No. 9-7e-22; Length 850; Matches 552; Conservative 33; Mismatches 43; Indels 22; Gaps 8;	DR	GO; GO:0005198; F:structural molecule activity; IEA.	
Query Match 3 LWVTTYYGVVWKEARATTFCASDAKAYTDEAHNVWATACVPTNPNOEVVLENVNEN 62	DR	InterPro; IPR000328; Env GP41.	
Matches 33 LWVTTYYGVVWKEARATTFCASDAKAYTDEAHNVWATACVPTDPNOEVVLENVNEN 92	DR	InterPro; IPR000777; GP120.	
Query 63 NMWQNNMVEONMHEIDILSDQSLKPCVKLPLCYTLNCSTDLNNTNTTELSLIVWWQ 122	DR	Pfam; PF00516; GP120; 1.	
Db 93 NMWQNNMVEONMHEIDILSDQSLKPCVKLPLCYTLNCSTDLNNTNTTELSLIVWWQ 146	DR	Pfam; PF00517; GP41; 1.	
Query 123 RGKGEMRNCSFNITTSIRDKVQREALEFYKLDEVIPDMDKNTNTKYLINGNTSITQ 182	KW	AIDS; Envelope protein; Transmembrane.	
Db 147 MERGIKNSCSFNITTSIRDKVQREALEFYKLDEVIPDMDKNTNTKYLINGNTSITQ 203	SEQUENCE	SEQUENCE 861 AA; 9831 MW; 4E8AF4276A9E302 CRC64;	
Query 183 ACPKVSFEPPIHYCTPTGPALKNDKEFNGTPCINSTVQOCTHIGRPVSTOLLING 242	Query	2 NLWVTVYGVVWKEARATTFCASDAKAYTDEAHNVWATACVPTNPNOEVVLENVNEN 61	
Db 204 ACPKVSFEPPIHYCTPAGFAILCKDKDFENGTPCINSTVQCTHIGRPVSTOLLING 263	Db	32 NLWVTVYGVVWKEARATTFCASDAKAYTDEAHNVWATACVPTDPNOEVVLENVNEN 91	
Query 243 SLAEEEVVIRSENFTNNAKTIIVOLANVSEBINCTRPNNTTRKRVTLGPRVYTTGELIG 302	Query	62 FNWKWKKNNVEQHEDISLWDOSLKPCKLPLCYTLNCSTDLNNTNTTELSLIVWWQ 121	
Db 264 SLABBEVVRSDFNFTDNAKTIIVOLQKESBINCTRPNNTTRKSITHGRAFTTGEIG 323	Db	92 FNWKWKKNNVEQHEDISLWDOSLKPCKLPLCYTLNCSTDLNNTNTTELSLIVWWQ 144	
Query 303 NIROHCN1SRAQNNNTLQQUATTLEREQFGNKTAENQSSGDPEIVMHSFNGGEFFYC 362	Query	122 ORGKEMERNCSFNITTSIRDKVQREALEFYKLDEVIPDMDKNTNTKYLINGNTSITQ 181	
Db 324 DIROHCN1SRAKVDNTLKVTRKLEREQGNKTIIVENQSSGDPEIVMHSFNGGEFFYC 383	Db	145 RENGEIKNCSCFNITTSIRDKVQREALEFYKLDEVIPDMDKNTNTKYLINGNTSITQ 201	
Query 363 NSTOLFNSAVWNT - SNGTWSVTBKQKDGTGDI - ITLPCKRIQKLNINRQWVGKAMYALPI 419	Query	182 OACPVSFEPPIHYCTPTGPALKNDKEFNGTPCINSTVQOCTHIGRPVSTOLLING 241	
Db 384 DSTQLFNSTWNTVETSNNNT-----EGNITITLPLCPRIQKQINNMQEVGKAMYAPIR 434	Db	202 QACPVSFEPPIHYCTPAGFAILCKDKDFENGTPCINSTVQOCTHIGRPVSTOLLING 261	
Query 420 GLIRGSSNTTGLLITRDGGENQTEIFRGGDMRDWRSELQYKVKIEPLGVAPT 479	Query	242 GSLAAEETVIRSENFTNNAKTIIVOLANVSEBINCTRPNNTTRKRVTLGPRVYTTGELIG 301	
Db 435 QIQRGSSNTTGLLITRDGGNESTEIFFPGGDMRDWRSELQYKVKIEPLGVAPT 494	Db	262 GSLAAEETVIRSENFTNNAKTIIVOLANVSEBINCTRPNNTTRKRVTLGPRVYTTGELIG 321	
Query 480 AKRERVQREKRAVGMFLGFLGAAGSTMAGTSMALTVQAQLLSGTIVQQQNLLRAI 539	Query	302 GNTRQAHEN1SRAQNNNTLQQUATTLEREQFGNKTAENQSSGDPEIVMHSFNGGEFFYC 360	
Db 495 AKRERVQREKRAVG-IGAYFLGFLGAAGSTMAGTSMALTVQAQLLSGTIVQQQNLLRAI 553	Db	322 GDTRQACNLTSRKWDTLKKVTKLGEQYGNNTK1VFNHSSGGDPDVIMSFNGGEFFP 381	
Query 540 KAQQHLLQLTWVGKIQQLQARILAVERYLKDQQLGFPGSGKLICITAPWNASWNKL 599	Query	361 YCNSTOLFNSAVWNTSNGTW----SVTRKQKDGTGDLITLPCRQKQLNINRQWVGKAMYA 415	
Db 554 EAQQHLLQLTWVGKIQQLQARILAVERYLKDQQLGFPGSGKLICITAPWNASWNKL 613	Db	382 YCNSTOLFNSWNE-NGTWNQNENNTWNNTPEGTNTDITLPCRQKQLNINRQWVGKAMYA 439	
Query 600 DQIWNNTMTEWNRDIEIDNYTHLYLIESQNOQEKKOELLDWKWASL 649	Query	416 LP1KG1LIRCSSNTTGLLITRDGGGE-NOTTELFRPGGDMRDWNWRELYKVKVKEPLG 474	
Db 614 DKIWNNTMTEWNRDIEIDNYTHLYLIESQNOQEKKOELLDWKWASL 663	Db	440 PPTRGQRCRSSNTTGLLITRDGGNGSRTTLEFRPGGDMRDWNWRELYKVKVKEPLG 499	
RESULT 12 Q7SUVA4_9HIV1 PRELIMINARY; PRT; 861 AA.	Query	475 VAPTKAKRVRVQREKRAVGMFLGFLGAAGSTMAGTSMALTVQAQLLSGTIVQQQN 534	
ID Q7SUVA4_9HIV1 PRELIMINARY;	Db	500 VAPTKAKRVRVQREKRAVGMFLGFLGAAGSTMAGTSMALTVQAQLLSGTIVQQQN 559	
AC Q7SUVA4_9HIV1 PRELIMINARY;	Query	535 LIRAIKAQOHLLQLTWVGKIQQLQARILAVERYLKDQQLGFPGSGKLICITAPWNASWN 594	
DT 01-OCT-2003 (TREMBirel. 25, Created)	Db	560 LIRAIKAQOHLLQLTWVGKIQQLQARILAVERYLKDQQLGFPGSGKLICITAPWNASWN 619	
DT 01-OCT-2003 (TREMBirel. 25, Last sequence update)	Query	595 SNKTLQDQ1WNNTMTEWNRDIEIDNYTHLYLIESQNOQEKKOELLDWKWASL 649	
DT 01-MAR-2004 (TREMBirel. 26, Last annotation update)	Db	620 SNRSLDD1WHNTWMWEREDNTSYLTYLIESQNOQEKKOELLDWKWASL 674	
DB Envelope glycoprotein.	DB	Name=env;	
OS Human immunodeficiency virus 1.	OC	Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;	
Lentivirus; Primate lentivirus group.	OC	RESULT 13 Q6UYP1_9HIV1	

ID	Q6UYBP1; 9HIV1 PRELIMINARY;	PRT;	867 AA.	Qy	534 NLIRAIKAQOHLLQITWNGIKOLQARILAVERYLKDOQLIGFWGGSGKLICCTTAPWNAS 593
AC	Q6UYBP1;			Db	573 NLLRAIEAQOHLLQITWNGIKOLQARILAVERYLRDQOQIIGWGGSKLICCTTAPWNAS 632
DT	05-JUL-2004 (TREMBirel. 27, Created)			Qy	594 WSNKTLQDQITWNNTMWEIDINTHLYLILBESQNOEKNQOBLLQDQKWL 649
RA	Kuhmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L., Snyder J., Riley J.M., Strick J.M., Baroudy B.M., Wilson I.A., Korber B.T., Wolinsky S.M., Moore J.P.;			Db	633 WSNISMSDE1WNNTMWEKEIDNTGILYLNLEKBSQNOEKNQOBLLQDQKWL 688
GN	Name-env;				
OS	Human immunodeficiency virus 1.				
OC	Virus; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae; Lentivirus; Primate lentivirus group.				
NCBI_TaxID	11676;				
OX					
RN					
RP					
RX					
PubRef=14980699; DOI=10.1128/JVI.78.6.2790-2807.2004;				Qy	534 NLIRAIKAQOHLLQITWNGIKOLQARILAVERYLKDOQLIGFWGGSGKLICCTTAPWNAS 593
RA	Kuhmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L., Snyder J., Riley J.M., Strick J.M., Baroudy B.M., Wilson I.A., Korber B.T., Wolinsky S.M., Moore J.P.;			Db	573 NLLRAIEAQOHLLQITWNGIKOLQARILAVERYLRDQOQIIGWGGSKLICCTTAPWNAS 632
RA	"Genetic and phenotypic analyses of human immunodeficiency virus type 1 escape from a small-molecule CCR5 inhibitor." J. Virol. 78:2790-2807(2004).			Qy	594 WSNKTLQDQITWNNTMWEIDINTHLYLILBESQNOEKNQOBLLQDQKWL 649
RT	EMBL; AY375550; AR00904.1; -; Genomic_DNA.			Db	633 WSNISMSDE1WNNTMWEKEIDNTGILYLNLEKBSQNOEKNQOBLLQDQKWL 688
RL	HSSP; P0478; PK33.				
SMR	06UYBP1; 93-147.				
DR	GO:0016021; C:Integral to membrane; IEA.				
DR	GO:0019031; C:Viral envelope; IEA.				
DR	GO:0005198; B:Structural molecule activity; IEA.				
DR	InterPro; IPR000777; GP120.				
DR	Pfam; PF00516; GP120; 1.				
DR	Pfam; PF00517; GP41; 1.				
DR	AIDS; Envelope protein; Transmembrane.				
FT	NON_TER; 1;				
SQ	SEQUENCE 867 AA; 98541 MW; F1F0B337BC7C6D CRC64;				
Query Match	83.3%; Score 2892.5; DB 2; Length 867;			Qy	3 LMWTTYYGYPWKEATTLEFCASDAKAYDTEAHNVWATHACVPTNPNOPEVVLENVTEN 62
Best Local Similarity	83.1%; Pred. No. 1.6e-220;			Db	33 LMWTTYYGYPWKEATTLEFCASDAKAYDTEAHNVWATHACVPTNPNOPEVVLENVTEN 92
Matches	545; Conservative 44; Mismatches 52; Indels 15; Gaps 8;			Qy	63 NMWKKNMVEOMHEIDISLNDQSLKFCVKLTPLCYTLCNTDL-NNTNT-TNTTELSIIVV 119
Qy	2 NLWWTYYGYPWKEATTLEFCASDAKAYDTEAHNVWATHACVPTNPNOPEVVLENVTEN 61			Db	93 NMWKKNMVEOMHEIDISLNDQSLKFCVKLTPLCYTLCNTLNRTNTNTSSG---- 148
Db	40 NLWWTYYGYPWKEATTLEFCASDAKAYDTEAHNVWATHACVPTDPNFOEVVLGNVTEN 99			Qy	120 WEQRKGEMRNCSPNITTSIRDYQREYALFYKDVDEPIDDNNKNTNTNNKTYRLNCNTSV 179
Qy	62 FNMWKNMVEOMHEIDISLNDQSLKFCVKLTPLCYTLCNTDL-TNTNTNTTELISIIVW 120			Db	149 WGE---EMTNCSFNITTSIRDYQREYALFYKDVDEPIDDNNKNTNTNNKTYRLNCNTSV 199
Db	100 FNMWKNMVGOMHEIDISLNDQSLKFCVKLTPLCYTLCNTDNNTNNANTNS----SW 154			Qy	180 ITOACPKVSPEPIPPIHYCPTGFLALLKCNDDKENGTPCTNVSTVQCTHIGRVYSTOLL 239
Qy	121 -EQRGKGMRCNSENITTSIRDYQREYALFYKDVDEPIDDNNKNTNTNNKTYRLNCNTSV 179			Db	200 ITQACPVSPEPIPPIHYCPTGFLALLKCNDDKENGTPCTNVSTVQCTHIGRVYSTOLL 259
Db	155 GEPMERGEKRNCSFNITTSIRDYQREYALFYKDVDEPIDDNNKNTNTNNKTYRLNCNTSV 214			Qy	300 ILMNTRQAHNCNISRAQWNNTLQQIATTLEHQFGNRTIAFNQSSGDPETVMHSFNCGGF 359
Qy	180 ITQACPVSPEPIPPIHYCPTGFLALLKCNDDKENGTPCTNVSTVQCTHIGRVYSTOLL 239			Db	320 IIGDRQAHNCNISRAQWNNTLQQIATTLEHQFGNRTIAFNQSSGDPETVMHSFNCGGF 379
Db	215 ITQACPVSPEPIPPIHYCAGAPEFAALKCNDDKENGTPCTNVSTVQCTHIGRVYSTOLL 274			Qy	360 FYCNSTOLFNSAWNTTSNQGNTIVQKQNTIVTWSVTRKQDGTGCTNVSTVQCTHIGRVYSTOLL 379
Qy	240 LNSLAAEEVYVIRSENFTNNAKTIVQVLLSVEINCTRPNHTRKVTLPGRVYTTGE 299			Db	380 FYCNSTOLFNSAWNTTSNQGNTIVQKQNTIVTWSVTRKQDGTGCTNVSTVQCTHIGRVYSTOLL 379
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Qy	300 IIGNRQAHNCNISRAQWNNTLQQIATTLEHQFGNRTIAFNQSSGDPETVMHSFNCGGF 358			Db	335 IIGDRQAHNCNISRAQWNNTLKHIVEKLQGOFQGNNTKTVNHSSCGDPETEMHSFNCGGF 394
Db	335 IIGDRQAHNCNISRAQWNNTLKHIVEKLQGOFQGNNTKTVNHSSCGDPETEMHSFNCGGF 394			Qy	359 FFYCNSTQLFNSKTFNISTW-TWINGTWTRANTERSNSTEEKITPLCKRQDGTGCTNVSTVQCTHIGRVYSTOLL 453
Qy	359 FFYCNSTQLFNSKTFNISTW-TWINGTWTRANTERSNSTEEKITPLCKRQDGTGCTNVSTVQCTHIGRVYSTOLL 453			Db	395 FFYKGRKCSNTGILITRDGGGENOT--TEIFRPGGGDMRDWRSELYKVKVPL 513
Db	454 FFYKGRKCSNTGILITRDGGGENOT--TEIFRPGGGDMRDWRSELYKVKVPL 513			Qy	411 PIKGJLRCSSNTGILITRDGGGENOT--TEIFRPGGGDMRDWRSELYKVKVPL 473
Qy	474 GVAPTKAKRKYQREKRAVGMFLGAAGTGMGATMSMALTQARQLLSGTIVQQQN 533			Db	442 AMYAPIKGLIRCSSNTGILITRDGGGENOT--TEIFRPGGGDMRDWRSELYKVKVPL 470
Db	426 AMYAPIRQGQIRCSSNTGILITRDGGGENOT--TEIFRPGGGDMRDWRSELYKVKVPL 485			Qy	474 GVAPTEAKRKYQREKRAVGMFLGAAGTGMGATMSMALTQARQLLSGTIVQQQN 572

Qy	471 EPLGYAPTKAKRKYVYREKRAVGMIGAMFLGFLGAGSTMGATSMALTYQARQLLSGVQ	530	Qy	300 ILGENIROAHCNISRAQWNTLQQIATTUREQFG_NKTIAPNQSSGGDPBEIVMEISFNCGGE	358
Db	486 EPLGYAPTKAKRKYVYREKRAVGMIGAMFLGFLGAGSTMGAAVALTYQARQLLSGVQ	545	Db	335 IIGDRIKAHCNISRAQWNTLKKVKEKGKOPGNNKTTIVENHSGGDPEIVMEISFNCGE	394
Qy	533 QQNLLRAIAQHQHQLQLTWIKOLQARLTLAVERYLKQOQLLGFWGCSGKLICCTTAVW	590	Qy	359 FFYCNSTQLENSAWNVTNGTWSV -TRKQDGTDITLPCRIKQINRWQVKGAMYAL 416	
Db	546 QQNLLRAIAQHQHQLQLTWIKOLQARLTLAVERYLKQOQLLGFWGCSGKLICCTTAVW	605	Db	395 FFYCNSTKLFNSTW -TRKQDGTDITLPCRIKQINRWQVKGAMYAP 453	
Qy	591 NASWNKTKTDQIWNMNTMNEWDRDNYTHLITYLIEEONQEQNQELLDKWASL 649		Qy	417 PIKGJRCSSNTGCLLITRDGGGENOT -TEIFRGGDMDRNWRSLEYKVKVKEPLGV 475	
Db	606 NASWNKSLNKIDWNMNTMWERETENYTSLVLTLYLIEEONQEQNQELLDKWASL 664		Db	454 PIREKIRCSNTGCLLITRDGGNDITSCEIFRGGDMDRNWRSLEYKVKVKEPLGI 513	
	RESULT 15		Qy	476 APIKAKRKYVOREKRAVGMIGAMFLGFLGAGSTMGATSMALTYQARQLLSGVQOQNNL	535
	Q6UTN6 9HIV1 PRELIMINARY;	PRT;	Qy	514 APIBAKRYVQREKRAVGMIGAMFLGFLGAGSTMGASVLTQARQLLSGVQOQNNL	572
	ID Q6UTN6;		Qy	536 LRAIKAOHLLQLTWIKOLQARLTLAVERYLKQOQLGFWGCSGKLICCTTAVPWNASW	595
AC	Q6UTN6;		Db	573 LRAIEAHOHLLQLTWIKOLQARLTLAVERYLKQOQLGFWGCSGKLICCTTAVPWNASW	632
DT	05-JUL-2004 (TREMBLrel. 27, Created)		Qy	596 NKTLQDNWNTMOMEWDIENDNTLYLTLIBESQNEQBNQBLILQDKNASL 649	
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)		Db	633 NKSMDIWNNTMOMEWEKDNTYGLTYNLLERSONQEQNEQELLADKWNAL 686	
DE	Envelope glycoprotein (Fragment).				
GN	Name=env;				
OS	Human immunodeficiency virus 1.				
OC	Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;				
OC	Lentiviruses; Primate lentivirus group.				
OX	NCBI TaxID:11676;				
	RP NUCLEOTIDE SEQUENCE.				
	Pubmed=14990659; DOI=10.1128/JVI.78.6.2790-2807.2004;				
RA	Kubmann S. E., Pugach P., Kurnstman K. J., Taylor J., Stanfield R. L.,				
RA	Stryder A., Strizik J. M., Riley J., Baroudy B. M., Wilson I. A.,				
RA	Korber B. T., Wolinsky S. M., Moore J. P.,				
RT	"Genetic and phenotypic analyses of human immunodeficiency virus type				
RT	1 escape from a small-molecule CCR5 inhibitor.";				
RL	J. Virol. 78:2790-2807(2004)				
DR	EMBL; A37555; AR00909; 1; -; Genomic_DNA.				
DR	SRB; Q6UTN6; 93-147, 557-641.				
DR	GO; GO:0016021; C:integral to membrane; IEA.				
DR	GO; GO:0019031; Viral envelope; IEA.				
DR	GO; GO:0005198; Protein structure, molecule activity; IEA.				
DR	InterPro; IPR000348; Env_Gp41.				
DR	InterPro; IPR000077; Gp120.				
DR	Pfam; PF00516; Gp120; 1.				
DR	Pfam; PF00517; Gp11; 1.				
DR	AIDS; Envelope protein; Transmembrane.				
FT	NON_TER 1				
SQ	SEQUENCE 865 AA: 9B421 MW: 9CB631053888BC207 CRC64;				
	Query Match 83.2%; Score 2889.5; DB 2; Length 865;				
	Best Local Similarity 83.0%; Pred. No. 2.7e-220; Indels 13; Gaps 8;				
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	62 FNNWKNMNMVEQMBEDIISWDSQSKPCVYLTPLCVTLNCTDLN-TANNTNTTELIIWW	120			
Db	100 FNNWKNMNMVEQMBEDIISWDSQSKPCVYLTPLCVTLNCTDLNCTNNNTATNSR----W	154			
Qy	121 -EQRGKGERMNCSENITTSIRDKVQREVALFYKLDVEPIDDNNKNTNTKYLJNCNTSV	179			
Db	155 GEPMEKGKEIKNCSFNITTSMRDKVQKDALFYKLDVVPIDKDSNNNTNTYNTLISCTNV	214			
Qy	180 ITQACPKVSEPIPHYCPTGPFALLKNDKKEFNGTGPCTNVSTVOCHTGTPVVSTOL	239			
Db	215 ITQACPKVSEPIPHYCPTGPFALLKNDKKEFNGTGPCTNVSTQCHTGTPVVSTOL	274			
Qy	240 LNGSLAEEPVVTESENFTNAKTTIVQUNVSVEINCRPNNTTRKRTLGPRVWTTGE	299			
Db	275 LNGSLAEEPVVTESENFTNAKTTIVQUNVSVEINCRPNNTTRKRTISMGRVLYTGE	334			

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OM protein - protein search, using sw model

Run on: March 7, 2006, 17:51:03 ; Search time 67.9631 Seconds

(without alignments)
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Scoring table: BLOSUM62

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Searched: 572060 seqs, 8275679 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2893.5	83.0	847	2 US-09-476-242-2	Sequence 2, Appli
2	2852	82.1	850	1 US-09-448-603A-28	Sequence 28, Appli
3	2852	82.1	850	2 US-09-434-075-28	Sequence 28, Appli
4	2852	82.1	850	2 US-09-492-739-28	Sequence 28, Appli
5	2852	82.1	850	2 US-09-966-931A-28	Sequence 28, Appli
6	2834	81.6	855	1 US-08-022-835-6	Sequence 6, Appli
7	2834	81.6	855	1 US-08-388-803-6	Sequence 6, Appli
8	2834	81.6	855	1 US-09-647-714-6	Sequence 6, Appli
9	2875.5	81.4	643	2 US-09-602-864-13	Sequence 13, Appli
10	2818	81.1	855	2 US-07-956-483-14	Sequence 14, Appli
11	2814.5	81.0	826	1 US-08-375-510-2	Sequence 2, Appli
12	2814.5	81.0	826	1 US-08-487-657-2	Sequence 2, Appli
13	2814.5	81.0	854	2 US-09-572-23	Sequence 23, Appli
14	2814.5	81.0	854	2 US-09-721-096-23	Sequence 23, Appli
15	2814	81.0	880	1 US-08-788-815-7	Sequence 7, Appli
16	2814	81.0	880	2 US-09-157-953-7	Sequence 7, Appli
17	2814	81.0	880	2 US-09-568-105-7	Sequence 7, Appli
18	2809.5	80.9	856	1 US-07-916-09A-2	Sequence 2, Appli
19	2809.5	80.9	856	2 US-09-476-242-1	Sequence 1, Appli
20	2809.5	80.9	857	1 US-09-448-603A-30	Sequence 30, Appli
21	2809.5	80.9	857	2 US-09-134-075-30	Sequence 30, Appli
22	2809.5	80.9	857	2 US-09-492-739-9	Sequence 30, Appli
23	2809.5	80.9	857	2 US-09-966-931A-30	Sequence 30, Appli
24	2807.5	80.8	855	2 US-07-935-433-15	Sequence 15, Appli
25	2806.5	80.8	856	2 US-09-124-900-9	Sequence 9, Appli
26	2806.5	80.8	863	2 US-08-463-210-11	Sequence 11, Appli
27	2806.5	80.8	863	2 US-08-463-028-11	Sequence 11, Appli

ALIGNMENTS

28	2806.5	80.8	863	2 US-08-463-209-11	Sequence 11, Appli
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31	2795	80.5	861	1 US-08-127-199A-14	Sequence 14, Appli
32	2795	80.5	861	1 US-08-482-847-14	Sequence 10, Appli
33	2795	80.5	861	2 US-07-956-483-10	Sequence 7, Appli
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35	2795	80.5	861	2 US-08-817-441-103	Sequence 13, Appli
36	2795	80.5	861	2 US-07-956-483-16	Sequence 5, Appli
37	2787	80.2	865	2 US-07-956-483-13	Sequence 32, Appli
38	2786.5	80.2	865	2 US-07-956-483-13	Sequence 32, Appli
39	2781.5	80.1	887	2 US-08-47-240A-5	Sequence 32, Appli
40	2781	80.1	665	1 US-08-148-603A-32	Sequence 32, Appli
41	2781	80.1	665	2 US-09-134-075-32	Sequence 32, Appli
42	2781	80.1	665	2 US-09-492-739-32	Sequence 32, Appli
43	2781	80.1	665	2 US-09-966-931A-32	Sequence 32, Appli
44	2780	80.0	657	2 US-09-256-194-2	Sequence 32, Appli
45	2772	79.8	635	2 US-09-536-977-68	Sequence 32, Appli

RESULTS

RESULT 1
US-09-476-242-2

; Sequence 2, Application US/09476242
 ; Patent No. 6889879
 ; GENERAL INFORMATION:
 ; APPLICANT: BARNETT, Susan
 ; APPLICANT: HARTOG, Karin
 ; APPLICANT: MARTIN, ERIC
 ; TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
 ; FILE REFERENCE: 1605.002
 ; CURRENT APPLICATION NUMBER: US/09/476,242
 ; CURRENT FILING DATE: 1999-12-30
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO: 2
 ; LENGTH: 847.
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus

US-09-476-242-2

Query	Match	Score	DB	Length
Query Match	83.0%	Score 2883.5;	DB 2;	Length 847;
Best Local Similarity	83.3%	Pred. No. 1.5e-229;		
Matches 544;	Conservative 40;	No. of mismatches 38;	Indels 31;	Gaps 7;
Qy	3	LWVTTYYGVPWKEATTLFCASDAKAYDTBAHNWATHACVPTNPQEVLENVNENF 62		
Db	33	LWVTTYYGVPWKEATTLFCASDAKAYDTBEVNTWATHACVPTPNQEVLENVNENF 92		
Qy	63	NMWNKMNVEQNHEDISLWQSLKCKVLTPLCYTLNCDLNTNTNTTELSTLUVVWEQ 122		
Db	93	NMWNKMNVEQNHEDISLWQSLKCKVLTPLCYTLHCT--NLKQATNKSSN---WE 146		
Qy	123	RGKGEMRNCNSFNITSIRDKVQEYALFYKLVDFDIDKKNNTNNTKYLNCTNTSVITQ 182		
Db	147	MDRGEIKNCFSFKVTTSTRNKMQEYALFYKLVDFDIDKKNNTNNTKYLNCTNTSVITQ 201		
Qy	183	ACPKYSFPPIPHTCPGPALLKNDKENGNTGCTNVSTVQCHGIRPVSTOLLNG 242		
Db	202	ACPKYSFPPIPHTCAPPAGEFLKNCNDKENGSGCTNVSTVQCHGIRPVSTOLLNG 261		
Qy	243	SLABEEVTRSENFTNAKNTVAKTIVOLANVSVEINCTPNNTRKTRVLYGPRWVYTGEILG 302		
Db	262	SLABEEVTRSENFTNAKNTVAKTIVOLANVSVEINCTPNNTRKTRVLYGPRWVYTGEILG 321		
Qy	303	NIROHCNTISRAONNTLQLQIAITLREQFGNKTAIPNQSSGGDPDVIMHSFNCGSEFFYC 362		
Db	322	DIROHCNTISGEKVNNTLQLQIVTKQAQFNSKNTKVFQKSSGGDPDVIMHSFNCGSEFFYC 381		
Qy	363	NSTQFNSAMVNT----SNGTWSVTRKQKDGTDLTPIKQITNRQVVGKAMYALP 417		

93 NMWNKINMVEQMHEDIISLWQDLSKPCVKLTPLCVTLNCCTL - KMATNTSSS ---WGK 146
 Db 382 NSTQLENSTWANTIGNNTG----- ITLP.CRIKQJINRROEVGKAMYAPP 428
 Qy 418 IKGLIRCSNITGILITRDGGGE-NOTTEI.FRPGGDMRDNWRSELYKKVKTEPLGA 476
 Db 429 IRGQIRCSNITGILITRDGGKEISNTTEI.FRPGGDMRDNWRSELYKKVKTEPLGA 488
 Qy 477 PTKAERKVREKRAVGMGLAMFGLAGAGSTMATSMALTVQRQLLGSIVQQNNIL 536
 Db 489 PTKAERKVREKRAVGMGLAMFGLAGAGSTMARSLTIVQRQLLGSIVQQNNIL 547
 Qy 537 RAIQAQHQLQLTWYKIKOQARLIAVERYLKDQQLLGFGCSKLICITTAAPVNAWSN 596
 Db 548 RAIEAQHQLQLTWYKIKOQARLIAVERYLKDQQLLGFGCSKLICITTAAPVNAWSN 607
 Qy 597 KTDQIWNNTWMEDREIDNYTHYLITYLLEESQNQEQKNQELQDQWLASL 649
 Db 608 KSDQIWNNTWMEDREIDNYTNUWEEQELDQQLLGFGCSKLICITTAAPVNAWSL 660

RESULT 2
 US 08-448-603A-28 ; Sequence 28, Application US/08448603A
 GENERAL INFORMATION:
 APPLICANT: Berman, Phillip W.
 APPLICANT: Nakamura, Gerald R.
 TITLE OF INVENTION: HIV Envelope Polypeptides
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
 STREET: 3 Embarcadero Center
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSQL for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/448, 603A
 FILING DATE: 07-JUN-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/072, 833
 FILING DATE: 07-JUN-93
 ATTORNEY/AGENT INFORMATION:
 NAME: Haliday, Emily
 REGISTRATION NUMBER: 38903
 REFERENCE/DOCKET NUMBER: 14918-704
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-393-2000
 TELEX: 415-393-2286

INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 850 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US -08-448-603A-28
 Query Match 62.1%; Score 2852; DB 1; Length 850;
 Best Local Similarity 83.0%; Pred. No. 6.2e-227; Mismatches 537; Conservative 42; Indels 16; Gaps 7;

94 NMWNKINMVEQMHEDIISLWQDLSKPCVKLTPLCVTLNCCTL - KMATNTSSS ---WGK 146
 Db 123 RGKGEMRNCSNITTSIRDVKORETALFYKLVTEPLGA 182
 Qy 147 MERGE1KNGSFNVTTSIRDVKMNEALFYKLVTEPLGA 201
 Db 183 ACPTVSFEPIPIHYCTPTGFALLKCNDKKFENGTPCTNYSVTOCHTGIRPVSTOLLNG 242
 Db 202 ACPTVSFEPIPIHYAPAGFAILCRDKCENGTCGCTAVSTVQCHGIRPVSTOLLNG 261
 Qy 243 SLAEEBVVIRSENFTNNAKTTIVOLQANVSBEINCPNNTTRKRVTLGPGRWYTTEPLG 302
 Db 262 SLAEEBVVRSANFDNAKTTIVOLQANESTVINC TRPNNNTTRSPGGRAFYANGTEPLG 321
 Qy 303 NIROHCNTSRAQWNTLQJATTREOFENKNTIAFNQSGGDPPIVMSFNCGEFFYC 362
 Db 322 DIROHCNLSSTKWNTLQJOUTKREHF NKTIVFHNSGGDPPIVMSFNCGEFFYC 380
 Qy 363 NSTOLFNSAWNNTSNTGWSVTRKQKDITLTPCRKOLINRQDQVKGAMYALPIKGLI 422
 Db 381 NTTPDENSTWNTY - TWANTEGSDMTGRNITLQCRKQLINNMGDEVGRAMYAPPQRGQI 438
 Qy 423 RCSSNITGILITRQGGENOTTEI.FRPGGDMRDNWRSELYKKVKTEPLGVATKAKR 482
 Db 439 RCSSNITGILITRD-GNNSETE.FRPGGDMRDNWRSELYKKVKTEPLGVATKAKR 497
 Qy 483 RVVQEKRAVGMGLAMFGLGAAGSTMATSMALTVQRQLLSIVQQONNLRAIKAQ 542
 Db 498 RVVQEKRAVG-IGMVELGPLGAAGSTMGAASVITVQRLLSGIVQQONNLRAIKEA 556
 Qy 543 QHLIQLTWYKIKOQARLIAVERYLKDQQLLGFWMCSGKLICITTAAPVNAWSNRTLDQI 602
 Db 557 QHLIQLTWYKIKOQARLIAVERYLKDQQLLGFWMCSGKLICITTAAPVNAWSNRSLDKI 616
 Qy 603 WNNMTWMEDREIDNYTHYLITYLLESQNQEQKNQELQDQWLASL 649
 Db 617 WDNTWMEWERETONYTSLIYSLIESQNQEQKNQELQDQWLASL 663

RESULT 3
 US-09-134-075-28
 ; Sequence 28, Application US/09134075
 ; Patent No. 6042836
 ; GENERAL INFORMATION:
 ; APPLICANT: Berman, Phillip W.
 ; APPLICANT: Nakamura, Gerald R.
 ; TITLE OF INVENTION: HIV Envelope Polypeptides
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
 ; STREET: 3 Embarcadero Center
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSQL for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/134, 075
 ; FILING DATE: 07-JUN-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/072, 833
 ; FILING DATE: 07-JUN-93
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Haliday, Emily
 ; REGISTRATION NUMBER: 38903
 ; REFERENCE/DOCKET NUMBER: 14918-704
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-393-2000
 ; TELEX: 415-393-2286
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 850 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US -08-448-603A-28
 ; Query Match 62.1%; Score 2852; DB 1; Length 850;
 ; Best Local Similarity 83.0%; Pred. No. 6.2e-227; Mismatches 537; Conservative 42; Indels 16; Gaps 7;
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/448, 603
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Haliday, Emily
 ; REGISTRATION NUMBER: 38903
 ; REFERENCE/DOCKET NUMBER: 14918-704
 ; TELEPHONE: 415-393-2000
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 850 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US -08-448-603A-28
 ; Query Match 62.1%; Score 2852; DB 1; Length 850;
 ; Best Local Similarity 83.0%; Pred. No. 6.2e-227; Mismatches 537; Conservative 42; Indels 16; Gaps 7;
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/448, 603
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Haliday, Emily
 ; REGISTRATION NUMBER: 38903
 ; REFERENCE/DOCKET NUMBER: 14918-704
 ; TELEPHONE: 415-393-2000
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 850 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US -08-448-603A-28
 ; Query Match 62.1%; Score 2852; DB 1; Length 850;
 ; Best Local Similarity 83.0%; Pred. No. 6.2e-227; Mismatches 537; Conservative 42; Indels 16; Gaps 7;

TELEFAX: 415-393-2286
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 850 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-134-075-28

Query Match Score 2852; DB 2; Length 850;
 Best Local Similarity 83.0%; Pred. No. 6.2e-227;
 Matches 537; Conservative 42; Mismatches 52; Indels 16; Gaps 7;

3 IAWTVYYGVPWKEATTLFCASDAKAYDTEAHNNWATHACYPNTNPQEVVLENTEVF 62
 Db 33 IAWTVYYGVPWKEATTLFCASDAKAYDTEAHNNWATHACYPNTNPQEVVLENTEVF 92
 Qy 63 NMWKDNMVEQMHEDISSLWDOSLKCPCVLTPLCVCVLTNCIDANTNTNTTELSTIIVWWEQ 122
 Db 93 NMWKDNMVEQMHEDISSLWDOSLKCPCVLTPLCVCVLTNCIDANTNTSSS---WKGK 146
 Qy 123 RGKGENRNCFSNITTSIRDKYOREALFYKLDVEPIDDKNTTNTKYLINNCNTSVTIQ 182
 Db 147 MERGBIKNCSPNVTISIRDKNKNEYALFYKLDVVDPN----DNTSYRLISCTNSVTIQ 201
 Qy 183 ACPKVSFEPIPHYCTPGLALKNDKCEKGNTGPTCNVNSTVQCTHIGIRPVSTOLLNG 242
 Db 202 ACPKVSFEPIPHYCTPAGFAILKCRDKFKTGPTCNVNSTVQCTHIGIRPVSTOLLNG 261
 Qy 243 SLABEEVVVIRSENFTNMAKTIIVQLNVSEINCTRPNNHTRKRYLGPGRWVYTGEILG 302
 Db 262 SLABEEVVVIRSANFDNAKTIIVQLNVSEINCTRPNNTRSIIHGRAFAYTGEIG 321
 Qy 303 NIROAHCNISRAQWNNTLQQATTLREQFGNKIAFNQSGGDPEIVMHSFNCGGEFFYC 362
 Db 322 DIRQAHCNLSSTKWNNTLKQIVTQVREHF-NKTTIVNHSSGGDPPEIVMHSFNCGGEFFYC 380
 Qy 363 NSTOLPNSAANVTSNGTWSYTRKDQTGDLTLPRIKQINRHWQVGKAMYALPIKGLI 422
 Db 381 NTTPLFNSTWNTY--TWNNTEGNSDTGRNLTQLCRKQIINMWQEVGKAMYAPIRGQI 438
 Qy 423 RCSSNITGLLITRDGGEGENQTEIFRGCGDMRDNWRSLEYKVKVKBPLGVAPTKAKR 482
 Db 439 RCSSNITGLLITRD-GGNNSETEIFRGCGDMRDNWRSLEYKVKVKBPLGVAPTKAKR 497
 Qy 483 RVMOREKRAYGMLGAMFLGFLGAGSTMAGTSMALTVQARQLLSGIVQOQNLLRAIKAQ 542
 Db 498 RVMOREKRAYV-IGAVFLGFLGAGSTMAGASVTLTVQARLLSGIVQOQNLLRAIKEAE 556
 Qy 543 OHLLQITWGKIKOLORAMILAVERYLKDQQLQGFWCGSKLICITAPWMAWSNKLDDQI 602
 Db 557 QHLLQITWGKIKQLQARLVAYERLYKDQQLQGFWCGSKLICITAPWMAWSNKLDDQI 616
 Qy 603 WNNMTWMEWDREIDNTYTHLTYLTLIBESQNQOEKNOELBLDKWASL 649
 Db 617 WDNNMTWMEWEIDNTSLISLISLBSQNQOEKNOELBLDKWASL 663

RESULT 4
 US-09-492-739-28
 Sequence 28, Application US/09492739
 Patent No. 6331404
 GENERAL INFORMATION:
 APPLICANT: Berman, Phillip W.
 Nakamura, Gerald R.
 TITLE OF INVENTION: HIV Envelope Polypeptides
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
 STREET: 3 Embarcadero Center
 CITY: San Francisco
 STATE: CA

COUNTRY: USA
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/492,739
 FILING DATE: 27-Jan-2000
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 09/134,075
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Haliday, Emily
 REGISTRATION NUMBER: 38903
 REFERENCE/DOCKET NUMBER: 14918-704
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-393-2000
 TELEFAX: 415-393-2286
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 850 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 US-09-492-739-28

Query Match Score 2852; DB 2; Length 850;
 Best Local Similarity 83.0%; Pred. No. 6.2e-227;
 Matches 537; Conservative 42; Mismatches 52; Indels 16; Gaps 7;
 Qy 3 LMWTVYYGVPWKEATTLFCASDAKAYDTEAHNNWATHACYPNTNPQEVVLENTEVF 62
 Db 33 LMWTVYYGVPWKEATTLFCASDAKAYDTEAHNNWATHACYPNTNPQEVVLENTEVF 92
 Qy 63 NMWKDNMVEQMHEDISSLWDOSLKCPCVLTPLCVCVLTNCIDANTNTTELSTIIVWWEQ 122
 Db 93 NMWKDNMVEQMHEDISSLWDOSLKCPCVLTPLCVCVLTNCIDANTNTSSS---WKGK 146
 Qy 123 LMWTVYYGVPWKEATTLFCASDAKAYDTEAHNNWATHACYPNTNPQEVVLENTEVF 182
 Db 147 LMWTVYYGVPWKEATTLFCASDAKAYDTEAHNNWATHACYPNTNPQEVVLENTEVF 201
 Qy 183 LMWTVYYGVPWKEATTLFCASDAKAYDTEAHNNWATHACYPNTNPQEVVLENTEVF 242
 Db 202 LMWTVYYGVPWKEATTLFCASDAKAYDTEAHNNWATHACYPNTNPQEVVLENTEVF 261
 Qy 243 LMWTVYYGVPWKEATTLFCASDAKAYDTEAHNNWATHACYPNTNPQEVVLENTEVF 302
 Db 262 LMWTVYYGVPWKEATTLFCASDAKAYDTEAHNNWATHACYPNTNPQEVVLENTEVF 321
 Qy 3 LMWTVYYGVPWKEATTLFCASDAKAYDTEAHNNWATHACYPNTNPQEVVLENTEVF 362
 Db 33 LMWTVYYGVPWKEATTLFCASDAKAYDTEAHNNWATHACYPNTNPQEVVLENTEVF 380
 Qy 63 NMWKDNMVEQMHEDISSLWDOSLKCPCVLTPLCVCVLTNCIDANTNTTELSTIIVWWEQ 122
 Db 93 NMWKDNMVEQMHEDISSLWDOSLKCPCVLTPLCVCVLTNCIDANTNTTELSTIIVWWEQ 146
 Db 123 RGKGENRNCFSNITTSIRDKYOREALFYKLDVEPIDDKNTTNTKYLINNCNTSVTIQ 182
 Db 147 MERGIIKNSFNTTSIRDKYOREALFYKLDVEPIDDKNTTNTKYLINNCNTSVTIQ 201
 Qy 183 ACPRVSFEPPIHYCTPGLALKNDKCEKGNTGPTCNVNSTVQCTHIGIRPVVSTOLLNG 242
 Db 202 ACPRVSFEPPIHYCTPGLALKNDKCEKGNTGPTCNVNSTVQCTHIGIRPVVSTOLLNG 261
 Qy 243 SLABEEVVVIRSENFTNMAKTIIVQLNVSEINCTRPNNHTRKRYLGPGRWVYTGEILG 302
 Db 262 SLABEEVVVIRSANFDNAKTIIVQLNVSEINCTRPNNTRSIIHGRAFAYTGEIG 321
 Qy 303 NIROAHCNISRAQWNNTLQQATTLREQFGNKIAFNQSGGDPEIVMHSFNCGGEFFYC 362
 Db 322 DIRQAHCNLSSTKWNNTLKQIVTQVREHF-NKTTIVNHSSGGDPPEIVMHSFNCGGEFFYC 380
 Qy 363 NSTOLPNSAANVTSNGTWSYTRKDQTGDLTLPRIKQINRHWQVGKAMYALPIKGLI 422
 Db 381 NTTPLFNSTWNTY--TWNNTEGNSDTGRNLTQLCRKQIINMWQEVGKAMYAPIRGQI 438
 Qy 423 RCSSNITGLLITRDGGEGENQTEIFRGCGDMRDNWRSLEYKVKVKBPLGVAPTKAKR 482
 Db 439 RCSSNITGLLITRD-GGNNSETEIFRGCGDMRDNWRSLEYKVKVKBPLGVAPTKAKR 497
 Qy 483 RVMOREKRAYGMLGAMFLGFLGAGSTMAGTSMALTVQARQLLSGIVQOQNLLRAIKAQ 542
 Db 498 RVMOREKRAYV-IGAVFLGFLGAGSTMAGASVTLTVQARLLSGIVQOQNLLRAIKEAE 556
 Qy 543 OHLLQITWGKIKOLORAMILAVERYLKDQQLQGFWCGSKLICITAPWMAWSNKLDDQI 602
 Db 557 QHLLQITWGKIKQLQARLVAYERLYKDQQLQGFWCGSKLICITAPWMAWSNKLDDQI 616
 Qy 603 WNNMTWMEWDREIDNTYTHLTYLTLIBESQNQOEKNOELBLDKWASL 649
 Db 617 WDNNMTWMEWEIDNTSLISLISLBSQNQOEKNOELBLDKWASL 663

RESULT 4
 US-09-492-739-28
 Sequence 28, Application US/09492739
 Patent No. 6331404
 GENERAL INFORMATION:
 APPLICANT: Berman, Phillip W.
 Nakamura, Gerald R.
 TITLE OF INVENTION: HIV Envelope Polypeptides
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
 STREET: 3 Embarcadero Center
 CITY: San Francisco
 STATE: CA

Db 557 QHLLQLTVWIKOLQARVLAVERYLKDQOLLIGIWCSCGLICITTAVPNNASNSNKLDDKI 616
 Qy 603 WNNNTWMEWDREIDNTYTHIYTIESONQOERKNOEELIOLDKWAISL 649
 Db 617 WDNNTWMEWEREIDNTTSIYTIESONQERNEQELIEDKWAISL 663

RESULT 5
 US-09-966-931A-28
 Sequence 28, Application US/09666931A
 Patent No. 606055
 GENERAL INFORMATION:
 APPLICANT: Berman, Phillip W.
 Nakanura, Gerald R.
 TITLE OF INVENTION: HIV Envelope Polypeptides
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
 STREET: 3 Embarcadero Center
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: PasteSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/966,931A
 FILING DATE: 27-Sep-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 09/492,739
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Haliday, Emily
 REGISTRATION NUMBER: 38903
 REFERENCE DOCKET NUMBER: 14918-704
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-393-2000
 TELEFAX: 415-393-2286
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 850 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 28:
 us-09-966-931A-28

Query Match Score 2852; DB 2; Length 850;
 Best Local Similarity 83.0%; Pred. No. 6.2e-227;
 Matches 537; Conservative 42; Mismatches 52; Indels 16; Gaps 7;

Qy 3 LWVTVYYGYPVWKEDATTUFCASDAKAVTDEAHNVWATHACVPTNPNOQEVVLENVNFF 62
 Db 33 LWVTVYYGYPVWKEDATTUFCASDAKAVTDEAHNVWATHACVPTNPNOQEVVLENVNFF 92
 Qy 63 NMWKNMNMVMEQMHEDISLDQSLKPCVKUTPLCYTLNCIDLNNTNTNTTELSLIVVWEQ 122
 Db 93 NMWKNMNMVMEQMHEDISLDQSLKPCVKUTPLCYTLNCIDLNNTNTNTTELSLIVVWEQ 146
 Db 33 RGKGEFRNCSEFNITSIRDKVQREVALYFLDVBPDNNKTNNTKYRLINGNTSVITQ 182
 Qy 147 MERGEIKNGSEFNITSIRDKMNEYALFYKLDDVPIDN----DNTSYRLISCNTSVITQ 201
 Qy 183 ACPKVSFEPIPBIHYCPTGPFALKCNDKKEFNGTGPCTNVSYTCGTHGIRPVSTOLLING 242
 Db 202 ACPKVSFEPIPBIHYCPTGPFALKCNDKKEFNGTGPCTNVSYTCGTHGIRPVSTOLLING 261
 Qy 243 SLAEEVVIRSENFTNNAAKTFIIVQLNVSBEINCRPNHHTRKVTLGPERWVYTGEIG 302

TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 JUS-08-022-835-6

	Query Match	Score	Length	DB 1;	DB 2;	DB 3;	DB 4;	DB 5;
	Best Local Similarity	81.6%	Score	2834;	DB 1;	Length	855;	
	Matches	534;	Pred. No.	1.9e-25;		Gaps	6;	
	Local Similarity	82.2%	Mismatches	53;	Indels	18;		
	Conservative	45;						
Dy	3 LWTWVYGPVWEATITLFCASDAKADTEAHNVWATHACVPTNPNEQEVLENNTNF	62						
Db	33 LWTWVYGPVWEATITLFCASBRKADTEEVNVWATHACVPTDPNPBEVLTNTNF	92						
Dy	63 NMWKNNMYEQMHEIIISLDQSLKPCVKLTPLCYTLNCTDLN--TN-NTTNTTTELTSIVV	119						
Db	93 NMWKNNMYEQMHEIIISLDQSLKPCVKLTPLCYTLNCTDLRATNGNDINTTSSRGMV	152						
Dy	120 WEQPGKGEMPNCSFNITISIRDKVQEKEYALFYKLDVEPIDDKNNTTNTKYKLINCTSV	179						
Db	153 ---GGEMKNCSFNITTNIRGKYQEKEYALFYKLDIAPIADNN---SNRYRLISCTNSV	204						
Dy	180 ITOACPYSPEPIHYCPTPTGFALLKCNKDENGKTPCPTINVSQTCQTCGIRPVSTQLL	239						
Db	205 ITOACPYSPEPIHYCAGPAFKLCDDKKGKGPCTNVSQTCQTCGIRPVSTQLL	264						
Dy	240 LNSLAAEEVVTSSENFTNAKTIIVOLNVSIEINCTRPNHTRTKRTVLGPGRVWYTTGE	299						
Db	265 LNSLAAEEVVVSANFADNAKVIVQINSVEINCTRPNNTKSIIHGPGRAFTTGEG	324						
Dy	300 ILGNIRQAHCNISPAQWNTILQQIATTYBQFGNKTAIFQNQSSGDEPYIMHSFNCGGF	359						
Db	325 IIQDIREQAHCNLSRAKWDTLNKLVIKLREQFGNKTIVPKHSSCDPEIVTHSNCGGF	384						
Dy	360 FYNNSTOLEPNSANVTSNNTWSVTRKQXDTGDIITLPCKIKOITIINRQVGKAMYALAPTK	419						
Db	385 FYNNSTQLINSTAVTVEENNTV----ENNITLPCRIKIQIINMWQVGRANTAPPTR	438						
Dy	420 GLIRCSNSNTGGLLTDGGGENOTTEIFPRGGGDMRDNNRSLEYKKVVKIEPLGVAPTK	479						
Db	439 GQTRCSNSNTGGLLTDGGSPEDNTKVRPRGGGDNMRDNNRSLEYKKVVKIEPLGVAPTK	498						
Dy	480 AKERVVQDKERKAVGMGANFLGFGAGSTGMGATSMALTVQARQLSGVQQQNLIRAI	539						
Db	499 AKERVVQDKERKAVG-IGAVFLGFLGAAGSTGMGAAMLTVQARULLSGIVQQQNLIRAI	557						
Dy	540 KAQQHLLOLTWVGKIQLOQARIAYERLYLKQDQLLGFMGSGLICITAIPWNASWSNKT	599						
Db	558 EAQHQHLLQITWVGKIQLQRVAYERLYLKQDQLLGFMGSGLICITAIPWNASWSNKL	617						
Dy	600 DQIWNNTMWMEDREIDNYNTLIVTLIERSQONQEQKNOQELLOLDKWAISL	649						
Db	618 NKIWDNTMTWIEDREINNTTSIIVSLLIESQONQEQKNEQELLDKWAISL	667						

RESULT 7

JUS-08-388-809-6

Sequence 6, Application US/08388809

Patent No. 5576000

GENERAL INFORMATION:

APPLICANT: REBITZ, JR., MARTIN S.; FRANCHINI, C.; MARGHAM, PHILIP D. GALLO, ROBERT C.; LORI, FRANCO C.; POPOVIC, MIKULAS; AND GARTNER, SUZANNE

ADDRESS: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

Qy 600 DQIWNMNTMWEWDRELDNTTHLYTTLIESONQOBKNOQELIQOLDKWA\$L 649
 Db 618 NKWIDMNTMWEWDRELNNTSISLIESONQOBKNEQELIQOLDKWA\$L 667

RESULT 8

US-08-647-714-6
 ; Sequence 6, Application US/08647714
 ; Patent No. 5869313

GENERAL INFORMATION:
 APPLICANT: REITZ, JR., MARVIN S.; FRANCHINT,
 GENOVEPPA, MARKHAM, PHILIP D; GALLO, ROBERT
 APPLICANT: C.; LORI, FRANCO C.; POPOVIC, MIKULLAS; AND
 APPLICANT: GARTNER, SUZANNE
 TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNEGAN
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK, 3.5"
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/647,714
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/388,809
 FILING DATE: 15-FEB-1995
 APPLICATION NUMBER: US 08/022,835
 FILING DATE: 25-FEB-1993
 APPLICATION NUMBER: US 07/599,491
 FILING DATE: 17-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: LESLIE A. SERONIAN
 REGISTRATION NUMBER: 35,353
 REFERENCE/DOCKET NUMBER: 2026-4092US2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 TELEX: 421792
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 855 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-647-714-6

Db 205 ITQACPVKVSEPIP HYCAPAGFALLKCKDKPFGIRPVYSTQVSTOLL 264
 Qy 240 LNGSLAAEEVVIIRSENFTINAKTTIVOLNVSUEINCTRNNHFKRKVTLGPGRVWYTTE 299
 Db 265 LNGSLAAEEVVIIRSFANFDNAKTVLQVOLNESVEINCTRNNNTKSIIHGPGRAFYTTCE 324
 Qy 300 ILGNTRQAHNISIAQWNTLQQATTIREQFGNKTIAFNQSSGDPETVMHSNCGGEF 359
 Db 325 IIGDQRQACNLSKPKWNTLINVTKIREQFGNKTIVKHSQCDPEVTHSPNCGGF 384
 Qy 360 FYCNSTOLENSANVNTSNGTWSVTRKQDTGDLITLPCRIKQIINRWQVKGAMYALPTK 419
 Db 385 FYCNSTQLENSTWNTVTEESNNTV -----BNNITLPCRIKQIINMWOFVGRMYAPPR 438
 Qy 420 GLIRCSSNTGLLITRDGGCENQTEIIFRGCGDMRDWRSELKVKVVKIEPLGVAPTK 479
 Db 439 GQLRCSSNTGLLITRDGGCENQTEVFRPGGDDMRDNWRSELKVKVVKIEPLGVAPTK 498
 Qy 480 AKRIVVQREKAVGMLGAMFLGFGLGAAGSTMGATSMALTVQAFQLSGIVQONNLIRAI 539
 Db 499 AKRIVVQREKAVG-IGAVPLGLQAASTMGAAHTLTQARULISGVQONNLIRAI 557
 Qy 540 KAQQHLLQLTWGIKQLRQLAVERYLKQDQQLGFGNGCSGKLICCTTAVPNNASWSNCTL 599
 Db 558 EAQQHLLQLTWGIKQLRQLAVERYLKQDQQLGIGWSGKLICCTTAVPNNASWSNCTL 617
 Qy 600 DQIWNMNTMWEWDRELDNTTHLYTTLIESONQOBKNEQELQDKWASL 649
 Db 618 NKWIDMNTMWEWDREBNNTSYIISLIESONQOBKNEQELQELDKWASL 667

RESULT 9
 US-09-602-864-13
 ; Sequence 13, Application US/09602864
 ; Patent No. 6710173
 ; GENERAL INFORMATION:
 ; APPLICANT: BINLEY, JAMES M
 ; APPLICANT: SCHUELKE, NORBERT
 ; APPLICANT: PAUL, WILLIAM C
 ; APPLICANT: PAUL, MADDON J
 ; APPLICANT: JOHN, MOORE P
 ; TITLE OF INVENTION: STABILIZED VIRAL ENVELOPE PROTEINS AND USES THEREOF
 ; FILE REFERENCE: 2048/59313.a
 ; CURRENT APPLICATION NUMBER: US/09/602,864
 ; CURRENT FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: 60/141,168
 ; PRIOR FILING DATE: 1999-06-25
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 13
 ; LENGTH: 643
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus type 1
 US-09-602-864-13

Query Match 81.4%; Score 2827.5; DB 2; Length 643;
 Best Local Similarity 82.2%; Pred. No. 4.5e-225; Mismatches 56; Indels 19; Gaps 4;
 Matches 532; Conservative 40; MisMatches 56; Indels 19; Gaps 4;

Qy 3 LWVTVYYGPVWKEATTIIFCASDAKAYTEAHNVWATHACVPTNPNQEYVILENTENF 62
 Db 33 LWVTVYYGPVWKEATTIIFCASDAKAYTEAHNVWATHACVPTDPNQEYVILENTENF 92

Qy 63 NMWKNNMVEQMHDISLWDQSLKPCVKLPLCYTLNCDTLNNTNTTELISIIVVWEQ 119
 Db 93 NMWKNNMVEQMHDISLWDQSLKPCVKLPLCYTLNCDTLNNTNTSSRQMV 152

Qy 120 WEQRGKGENRNCNFNTTSITRDYKOREYALPKUDVPTDNTNTNTKYRLNNTSIVTQ 179
 Db 133 LWVTVYYGPVWKEATTIIFCASDAKAYTEAHNVWATHACVPTDPNQEYVILENTENF 92

Qy 123 RGKGEHRNCNFNTTSITRDYKOREYALPKUDVPTDNTNTNTKYRLNNTSIVTQ 182
 Db 118 -EGEIKNCNFNTTSIRDEVQKEYLFYKLDVPDN----NNTSYRLISCDTYSVITQ 171

Qy 180 ITQACPVKVSEPIP HYCAPAGFALLKCKDKPFGIRPVYSTQVSTOLL 239

Db 172 ACPKISFEPPIHYCAPAGFAILPKNDKTFNGKGPCKNVSTVQCTHIGIRPVVSTOLLING 231 ;
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-07-956-483-14

Qy 243 SLAEEFTVIRSENFTNAKTTIIVQLANVSVEINCTRPNHNPTRKRVTLGPRVWYTGEIGL 302 ;
 ;
 Db 232 SLAEEFTVIRSDNFTNAKTTIIVOLKESTEINCTRPNNTNRKSTHIGPRAFYTGTEIG 291 ;
 ;
 Qy 303 NIROAHCNISRAQWNNTLQQIATTAREQFGNKTAIFANQSSCGDPEVMMHSFNCGEFFYC 362 ;
 ;
 Db 292 DIROAHCNISRAKNDTLLQVIKLREQFENKTIIVPHSSCGDPEVMMHSFNCGEFFYC 351 ;
 ;
 Qy 363 NSTOLFNSAWNTVTSNGTWSTTRKQDGTDLTLPCKIQKLINRQWVQVGKAMYALPIKGII 422 ;
 ;
 Db 352 NSTQLENSTWNNTIEGS-----NNTGENTLTLPCKIQKLINMWWGKVAMYAPPGRQI 405 ;
 ;
 Qy 423 RCSSNITGLLTRDGGENQTEIIPPGGDMRDWRSELYKVKVTKIPGVAPTKAKR 482 ;
 ;
 Db 406 RCSSNITGLLTRDGGENQTEIIPPGGDMRDWRSEFYKVKVVKIPGVAPTKCR 465 ;
 ;
 Qy 483 RVVQREKRAVGMLGAMFLGFLGAAGSTMGATSMALTVQAROLLSGVVOQVNLLIRAKQ 542 ;
 ;
 Db 466 RVVQREKRAVG-IGAVFLGFLGAAGSTMGAASMTLTVQARLLSGTVQVNLLIRATEAQ 524 ;
 ;
 Qy 543 QHLLQLTWGIKQLOQARLIALVERYLKDQQLIGFWGCGSGKLICITTAAPVNNASWNKTLDOI 602 ;
 ;
 Db 525 QRMLQLTWWGIKQLOQARLIALVERYLGDQQLIGWGCGSGKLICCTAVPNNASWNKSLDR 584 ;
 ;
 Qy 603 WNNNTTMEWDEBDINTHTLITLIESNOQERNOELQOLDKWSL 649 ;
 ;
 Db 585 WNNNTTMEWEREIDNTYSETIXLIESQNQEKNEQELLDKWSL 631 ;
 ;
 RESULT 10
 US-07-956-483-14
 Sequence 14, Application US/07956483
 Patent No. 6761799
 GENERAL INFORMATION:
 APPLICANT: KLENY, Marie-Paule
 TITLE OF INVENTION: NOVEL HYBRID, SOLUBLE AND UNCLEAVED
 TITLE OF INVENTION: gp160 VARIANT
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Burns, Doane, Swecker & Mathis
 STREET: P.O. Box 1404
 CITY: Alexandria
 STATE: Virginia
 COUNTRY: United States
 ZIP: 22313-1404
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/956,483
 FILING DATE: 31-DEC-1992
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO 92/19742
 FILING DATE: 12-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PR 91 05392
 FILING DATE: 02-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Crane-Feury, Sharon E
 REGISTRATION NUMBER: 36,113
 REFERENCE/DOCKET NUMBER: 017753-005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-6620
 TELEX/FAX: (703) 836-2021
 SEQUENCE FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 855 amino acids
 TYPE: amino acid

Db 381 FYCNSTOLFSSTWNTGEGSNNTGG-----NDITLPLRIKEINMWDGVKAMYAPP 432 ;
 ;
 Qy 418 IKGLJIRCSSNTGLLTRDG-----GGENOTTELFRPGGGADMRDWNRSLEYKVKVIEP 472 ;
 ;
 Db 433 IKGQTKCSSNTGLLTRDGNSKNGSQNTEFRPGGGADMRDWNRSLEYKVKVIEP 492 ;
 ;
 Qy 473 LGVAPTKAKRVRVQEKEKRAVGMGLGAGSTMGATSMALTVQARLLSGIVQQ 532 ;
 ;
 Db 493 LGVAPTKAKRVRVQEKEKRAVGTIGMFLGFLGANGSTMGATSMVQARLLSGIVQQ 552 ;
 ;
 Qy 533 NNLRIAKIAQHLLQDQQLGFWGCGSGKLICITPAVNNA 592 ;
 ;
 Db 553 NNLRIAEQAQHLLQDQQLGFWGCGSGKLICITVPMT 612 ;
 ;
 Qy 593 SWSNTLQD1WNNTMMDREIDNTYLIYLIESQEQKNQELQDKWASL 649 ;
 ;
 Db 613 SWSNKSLLD1WGNNTMWEERETIYNTSLIYLIESQEQKNQELLDKWASL 669 ;
 ;
 RESULT 11
 US-08-375-510-2
 Sequence 2, Application US/08375510
 Patent No. 5576421
 GENERAL INFORMATION:
 APPLICANT: Saito, Atsushi
 APPLICANT: Sinagawa, Hideo
 APPLICANT: Nakata, Atsuo
 TITLE OF INVENTION: HIV ANTIGEN
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Birch, Stewart, Kolasch and Birch
 STREET: P.O. Box 747
 CITY: Falls Church
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22040-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 04-DEC-1992
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/985, 949
 FILING DATE: 04-DEC-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Svensson, Leonard R.
 REGISTRATION NUMBER: 30,330
 REFERENCE/DOCKET NUMBER: 216-309P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 241-1300
 TELEX: 248345
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 826 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-375-510-2

Query Match 81.0%; Score 2814.5; DB 1; Length 826;
 Best Local Similarity 82.9%; Pred. No. 7.4e-224;
 Matches 540; Conservative 34; Mismatches 56; Indels 21; Gaps 9;

Qy 3 LAVVYYGVPWKEATTIIFCASDAKAYTDEAHNWATHACVPTNPNNPQEVLNTENP 62
 Db 6 LAVVYYGVPWKEATTIIFCASDAKAYTDEAHNWATHACVPTDPNPEQVVLVNNTENP 65

Qy 63 NMWKNNMVBONHEDILSMWQSLKEPCVKLTPLCYTLNCPTDLNTNTNTTELSTIIVWFO 122
 Db 66 NMWKNDMVEQMHEDEIISLWQSLKEPCVKLTPLCYTLNCPTDLNTNTNTTELSTIIVWFO 122

Qy 123 RGKGERMNCFSNITTSIRDKVQREYALFYKLQDVEPIDDNKNTNTKCYPLNCNTSIVTQ 182
 Db 123 --KGELIKNCFSNITTSIRDKVQKEYAFFYKLQDVIDP-----NTSYRLISCTNSIVTQ 173

Qy 183 ACPKVSFEPPIPHYCTPTGPFALLKNDKCFENGTCPTCNVSTVQTHGIPRPPVSTOLLING 242
 Db 174 ACPKVSFEPPIPHYCAPKNNKCFENGTCPTCNVSTVQTHGIPRPPVSTOLLING 233

Qy 243 SLAEEVVVISENFTNNAKTIIVQNVSLQIAATTLRQEFQ-NKTIATFQNSGGDPEIYMHSEFGGF 300
 Db 234 SLAEEVVVISANFTDNAKTIIVQNTSTEVINCRPNNTRKSRIQQRPGRAVTIGI 293

Qy 301 LGNTROAHCNTRSAQMNNTLQIAATTLRQEFQ-NKTIATFQNSGGDPEIYMHSEFGGF 359
 Db 294 -GNMROAHCNTRSAKWNATLQIAASKLREOFGNNTKIPKQSGGDPEIYVTHSEFGGF 352

Qy 360 FYCNSTQLFISAWNTVNGWSVTRVKQKOTG-DLTLPCKRIQKINRNQVQGKMYALFI 418
 Db 353 FYCNSTQLFNSTW--FNSTWSTEGSNNTTEGSDTITLPCKRIQFNMQVQVGKAMYAPI 409

Qy 419 KGLIRCSSNTGLLTDQGENOTTEIIPPGGDMRDWRSELVYKVVKIBPLGVRAFT 478
 Db 410 SGQIIRCSSNTGLLTDQGENOTTEIIPPGGDMRDWRSELVYKVVKIBPLGVRAFT 469

Qy 479 KAKRRVQREKRAVEMLGAMFLGLGAAGSTMGMATSMAALTVQAROLLSGIVOCQNNLLRA 538
 Db 470 KAKRRVQREKRAV-IGALFLGLGAAGSTMGTSMTIVTQAROLLSGIVOCQNNLLRA 528

Qy 539 IKAQHLLQLTWYGIKQIQLQARIЛАВЕРҮЛДQOQIGFWGCSGKLUICRT2AVPMNASWNKT 598
 Db 529 IEAQHLLQLTWGIKQIQLQARIЛАВЕРҮЛДQOQIGFWGCSGKLUICRT2AVPMNASWNKT 588

Qy 599 LDQIWNNTMWEDEIDNYTHLTYLIESBONQEKNOQELLOLDKWAISL 649
 Db 589 LEQIWNNTMWEDEIDNYTHLTYLIESBONQEKNOQELLOLDKWAISL 639

RESULT 12
 US-08-48-657-2 ; Sequence 2, Application US/08487657
 ; Patent No. 583467
 GENERAL INFORMATION:
 APPLICANT: Saito, Atsushi
 APPLICANT: Sinagawa, Hideo
 APPLICANT: Nakata, Atsuo
 TITLE OF INVENTION: HIV ANTIGEN
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Birch, Stewart, Koliasch and Birch
 STREET: P.O. Box 747
 CITY: Falls Church
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22040-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487, 657
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/375, 510
 FILING DATE: 18-JAN-1995
 APPLICATION NUMBER: US/07/985, 949
 FILING DATE: 04-DEC-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Svensson, Leonard R.
 REGISTRATION NUMBER: 30,330
 REFERENCE/DOCKET NUMBER: 216-309P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 241-1300
 TELEFAX: (703) 241-2848
 TELEX: 248345
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 826 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-487-657-2

Query Match 81.0%; Score 2814.5; DB 1; Length 826;
 Best Local Similarity 82.9%; Pred. No. 7.4e-224;
 Matches 540; Conservative 34; Mismatches 56; Indels 21; Gaps 9;

Qy 3 LAVVYYGVPWKEATTIIFCASDAKAYTDEAHNWATHACVPTNPNNPQEVLNTENP 62
 Db 6 LAVVYYGVPWKEATTIIFCASDAKAYTDEAHNWATHACVPTDPNPEQVVLVNNTENP 65

Qy 63 NMWKNNMVBONHEDILSMWQSLKEPCVKLTPLCYTLNCPTDLNTNTNTTELSTIIVWFO 122
 Db 66 NMWKNDMVEQMHEDEIISLWQSLKEPCVKLTPLCYTLNCPTDLNTNTNTTELSTIIVWFO 122

Qy 123 RGKGERMNCFSNITTSIRDKVQREYALFYKLQDVEPIDDNKNTNTKCYPLNCNTSIVTQ 182
 Db 123 --KGELIKNCFSNITTSIRDKVQKEYAFFYKLQDVIDP-----NTSYRLISCTNSIVTQ 173

Qy 183 ACPKVSFEPPIPHYCTPTGPFALLKNDKCFENGTCPTCNVSTVQTHGIPRPPVSTOLLING 242
 Db 174 ACPKVSFEPPIPHYCAPKNNKCFENGTCPTCNVSTVQTHGIPRPPVSTOLLING 233

Qy 243 SLAEEVVVISENFTNNAKTIIVQNVSLQIAATTLRQEFQ-NKTIATFQNSGGDPEIYMHSEFGGF 300
 Db 234 SLAEEVVVISANFTDNAKTIIVQNTSTEVINCRPNNTRKSRIQQRPGRAVTIGI 293

Qy 301 LGNTROAHCNTRSAQMNNTLQIAATTLRQEFQ-NKTIATFQNSGGDPEIYMHSEFGGF 359
 Db 294 -GNMROAHCNTRSAKWNATLQIAASKLREOFGNNTKIPKQSGGDPEIYVTHSEFGGF 352

Qy 360 FYCNSTQLFISAWNTVNGWSVTRVKQKOTG-DLTLPCKRIQKINRNQVQGKMYALFI 418
 Db 353 FYCNSTQLFNSTW--FNSTWSTEGSNNTTEGSDTITLPCKRIQFNMQVQVGKAMYAPI 409

Qy 419 KGLIRCSSNTGLLTDQGENOTTEIIPPGGDMRDWRSELVYKVVKIBPLGVRAFT 478
 Db 410 SGQIIRCSSNTGLLTDQGENOTTEIIPPGGDMRDWRSELVYKVVKIBPLGVRAFT 469

Qy 479 KAKRRVQREKRAVEMLGAMFLGLGAAGSTMGMATSMAALTVQAROLLSGIVOCQNNLLRA 538
 Db 470 KAKRRVQREKRAV-IGALFLGLGAAGSTMGTSMTIVTQAROLLSGIVOCQNNLLRA 528

Qy 539 IKAQHLLQLTWYGIKQIQLQARIЛАВЕРҮЛДQOQIGFWGCSGKLUICRT2AVPMNASWNKT 598
 Db 529 IEAQHLLQLTWGIKQIQLQARIЛАВЕРҮЛДQOQIGFWGCSGKLUICRT2AVPMNASWNKT 588

1744 ACPKVSPEPIP HYCAPAGPAILCKCNKNPKTFNGTGPCTNVQTHGIRPVSTOLLING 233
 243 SLAEEVVIRSENFTNNAKTTIVQLNVSEVINC TRPNHTRK--RVTLGGRWVTTGZI 300
 243 SLAEEVVVIRSENFTNNAKTTIVQLNVSEVINC TRPNHTRK--RVTLGGRWVTTGZI 300
 244 SLAEDDVVLRSAFTNAKTTIVQLNTSEVINC TRPNHTRKSLRQGGRAFTVIGKI 293
 301 LGNTROAHCNISRAQWNNTLQIAUTLRLBORG-NKTLIAFNQSSGDPETWHSFNCGBF 359
 294 -GNMRQAHCNISRAQWNNTLQIAUTLRLBORG-NKTLIAFNQSSGDPETWHSFNCGBF 359
 360 FYCNSTOLFNSAWNTSNGTWSVTRKQDKT-DITLPCRIKQIINRWQVKGAMYALPI 418
 353 FYCNSTOLFNSAWNTSNGTWSVTRKQDKT-DITLPCRIKQFNMWQVGKAMYAPPI 409
 419 KGLIRCSSNITGLLTRDGGENOTTEIFRGGDMRDNRSELKYKVKYKIEPLGVAPT 478
 400 SGQIRCSSNITGLLTRDGGNNNSSEIFRGGDMRDNRSELKYKVKYKIEPLGVAPT 469
 410 KAKRVRVQREKRAVGMGLGAMFLGFQAAGSTMGATSMALTYQARQLSMGTSGVQQLNLRA 538
 479 KAKRVRVQREKRAVGMGLGAMFLGFQAAGSTMGATSMALTYQARQLSMGTSGVQQLNLRA 538
 470 KAKRVRVQREKRAVGMGLGAMFLGFQAAGSTMGATSMALTYQARQLSMGTSGVQQLNLRA 528
 539 IKAQHLLQLTVWGIKQLOARI LAVERYLKDQQLIGWGSGLKLCITTA PWNAWSNKT 598
 529 IEAQHLLQLTVWGIKQLOARI LAVERYLKDQQLIGWGSGLKLCITTA PWNAWSNKS 588
 599 LDQIWNNTMNEWDRIDNTYLITYLIESQNOEKNOQELLDKWL 649
 617 LEQIWNNTMNEWDRIBINNTSLHSLIESQNOEKNEQELLDKWL 619
 589 LEQIWNNTMNEWDRIBINNTSLHSLIESQNOEKNEQELLDKWL 639

RESULT 14

US-09-718-096-23

; Sequence 23, Application US/09718096

; Patent No. 6589763

; GENERAL INFORMATION:

; APPLICANT: Von Laer, Meike-Dorothee

; TITLE OF INVENTION: RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH LCMV

; FILE REFERENCE: 35-195

; CURRENT APPLICATION NUMBER: US/09/718,096

; PRIORITY NUMBER: DE 19856163.5

; PRIOR FILING DATE: 1998-11-26

; PRIOR APPLICATION NUMBER: EP 99250415.9

; PRIOR FILING DATE: 1999-11-25

; PRIOR APPLICATION NUMBER: US 09/309,572

; PRIOR FILING DATE: 1998-11-26

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 23

; LENGTH: 854

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

; FEATURE: envelope polyprotein

; OTHER INFORMATION: envelope polyprotein

US-09-718-096-23

RESULT 13

US-09-309-572-23

; Sequence 23, Application US/09309572

; Patient No. 6440730

; GENERAL INFORMATION:

; APPLICANT: Heinrich-Pette-Institut

; TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV

; FILE REFERENCE: P5049

; CURRENT APPLICATION NUMBER: US/09/309,572

; CURRENT FILING DATE: 1999-05-11

; EARLIER APPLICATION NUMBER: DE 199 56 463

; EARLIER FILING DATE: 1998-11-26

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 23

; LENGTH: 854

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

; FEATURE: envelope polyprotein

; OTHER INFORMATION: envelope polyprotein

US-09-309-572-23

Query Match 81.0%; Score 2814.5; DB 2; Length 854;
 Best Local Similarity 82.9%; Pred. No. 7.8e-224; Matches 540; Conservative 34; Mismatches 56; Indels 21; Gaps 9;

3 LWVTTYYGVPWKCAATTTCASDAKAYTDEARNWATHACVPTNPNPQBVLENVNINF 93
 34 LWVTTYYGVPWKCAATTTCASDAKAYTDEARNWATHACVPTNPNPQBVLENVNINF 62
 34 LWVTTYYGVPWKCAATTTCASDAKAYTDEARNWATHACVPTNPNPQBVLENVNINF 62
 63 NMWKNMVEQMHD1ISLNDQSLKPCVKLTPLCYTLCDLNNTNTTELIVVWQ 122
 94 NMWKNMVEQMHD1ISLNDQSLKPCVKLTPLCYTLCDLNNTNTTELIVVWQ 122
 123 RGKEGMRSNFSNITSIRDKVQEVALFKLDEVPTDDNNTNTKYLINCNTSVITQ 182
 151 -KGEIKKNSFNITSIRDKVQEAFYKLIDVIP-----NTSYFLISCNTSVITQ 201
 183 ACPKVSPEPIP HYCAPAGPAILCKCNKNPKTFNGTGPCTNYSTVQTHGIRPVSTOLLING 242
 202 ACPKVSPEPIP HYCAPAGPAILCKCNKNPKTFNGTGPCTNYSTVQTHGIRPVSTOLLING 261

DDB	202	ACPKVSEPIPHYCAPAGFAILKCNKNITFNGTGPCTNVSTVQCTHGRPVVSTQLLING	261	; LENGTH: 880 amino acids
QY	243	SLAEEVVIRSENFTNNAMTIIVOLNVSVEINCTRPNHTRK--RVTLGPGRYWTGEEI	300	; TYPE: amino acid
DDB	262	SLAEEVVIRSANFTDNATKIVQLNTSVEINCTRPNNTRKSRIQGPGRAFTICKI	321	; STRANDEDNESS: both
DDB	270	US-08-788-815-7		; TOPOLOGY: both
DY	301	LGNTRQAHNCISRAQWNNTLQQIAATTLRPQG-NKTIANFQNSSGDPEIVMASFNCGEF	359	; MOLECULE TYPE: protein
DDB	322	-GNMRQAHNCISRAKWNATLKQASKLREQFGNNKTIIFKQSSGGDPPEVTHSFNCGEF	380	
DY	360	FYCNSTOLFNSAANVTSNGTWSVTRKOKDTG-DITLPLCRIKOINRQVYGRAMYALPI	418	
DDB	381	FYCNSTQLNSTW--FNNTWSTEGSNTTEGSDTITLPERIKOFINNMQEVGRAMYAPI	437	
DY	419	KGLIRCSSNITGGLLTDQGGENOTTEIFTRPGGDMDRNWRSELKYKVKEIPLGVAPT	478	
DDB	438	SGQTRCSNSNITGGLLTDQGNNNGSEIFTRPGGDMDRNWRSELKYKVKEIPLGVAPT	497	
DY	479	KAGRVRVOREKRAVGMFLGFLGAACSTMGMATSMWLTVAQRQLISGTVOCQNNLIR	538	
DDB	498	KAGRVRVOREKRAV-IGFLGFLGAACSTMGMCTSMWLTVAQRQLLSIVOCQNNLIR	556	
DY	539	TKAQHQHLLCUTVNGIKOLQARILAVERYLKDDQQLGPGCSGKLICCTAVPNASWSNK	598	
DDB	557	IEAQHQHLLCUTVNGIKOLQARILAVERYLKDDQQLGPGCSGKLICCTAVPNASWSNK	616	
DY	599	LDQIWNNTMWMENDREIDNTLJYTLLIESONQEKNQELQLDKWASL	649	
DDB	617	LEQIWNNTMWMENDREINNTSLHSLLIESONQEKNQELQELLDKWASL	667	
DY	RESULT 15			
DDB	7	Sequence 7, Application US/08788815		
DDB	5846546	Patent No.		
DY	GENERAL INFORMATION			
DDB	St. Jude Children's Research Hospital			
DDB	332 No. 584654666 Lauderdale			
DDB	PO Box 318			
DDB	United States of America			
DDB	Collection, Christopher			
DDB	Owens, Randall J.			
DDB	Slabod, Karen			
DDB	PREPARATION AND USE OF VIRAL VECTORS FOR			
DDB	TITLE OF INVENTION:	MIXED ENVELOPE PROTEIN VACCINES AGAINST HUMAN		
DDB	TITLE OF INVENTION:	IMMUNODEFICIENCY VIRUS		
DDB	NUMBER OF SEQUENCES:	7		
DDB	CORRESPONDENCE ADDRESS:			
DDB	ADDRESSEE: KLAUBER & JACKSON			
DDB	STREET: 411 HACKENSACK AVENUE			
DDB	CITY: HACKENSACK			
DDB	STATE: NJ			
DDB	COUNTRY: USA			
DDB	532 QNNLRLATAQOHLQILTWGIKLQARILAYERLYKDQQLGFWGCGSKLICITVAPWN	591		
DDB	576 QNNLRLATEAOQLLQILTWGIKLQARILAYERLYKDQQLGTWGCGSKLICITVAPWN	635		
DY	592 ASNSNKTLDQIWNNTMWNEDREI1DNTLHYLTLIESQNQEQKNQEQELLDQKWLASL	649		
DDB	636 ASWSNSKSLQIWNNTMWNEDREI1NNTSLHJLIESQNQEQKNQEQELLDQKWLASL	693		

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OM protein - protein search, using sw model

Run on: March 7, 2006, 17:51:52 ; Search time 211.547 Seconds

(without alignments)

1281.847 Million cell updates/sec

Title: US-09-938-406-1_COPY_33_681

Perfect score: 34 74

Sequence: 1 ANLWVTVYGYPVWKBEATT.....QNQQBXNQQELLQDQKWAISL 649

Scoring table: BLUSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters:

1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : Published_Applications_AA_Main:
 1: /cgn2_6/podata/1/pubpaas/US07_PUBCOMB.pep:
 2: /cgn2_6/podata/1/pubpaas/US08_PUBCOMB.pep:
 3: /cgn2_6/podata/1/pubpaas/US09_PUBCOMB.pep:
 4: /cgn2_6/podata/1/pubpaas/US10_PUBCOMB.pep:
 5: /cgn2_6/podata/1/pubpaas/US10B_PUBCOMB.pep:
 6: /cgn2_6/podata/1/pubpaas/US11_PUBCOMB.pep:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	3.474	100.0	868	3	US-09-938-406-1	Sequence 1, Appli
2	2.987	85.0	862	5	US-10-780-507-51	Sequence 51, Appli
3	2.977.5	85.7	883	4	US-10-441-926-2	Sequence 2, Appli
4	2.977.5	85.7	883	4	US-10-441-949-2	Sequence 2, Appli
5	2.977.5	85.7	883	5	US-10-780-507-2	Sequence 2, Appli
6	2.977.5	85.7	883	5	US-10-780-507-121	Sequence 121, Appli
7	2.949	84.9	862	5	US-10-780-507-50	Sequence 50, Appli
8	2.896.5	83.4	852	4	US-10-093-553A-29	Sequence 2, Appli
9	2.883.5	83.0	842	4	US-10-190-435-2	Sequence 2, Appli
10	2.883.5	83.0	842	4	US-10-241-009-2	Sequence 2, Appli
11	2.883.5	83.0	842	4	US-10-190-434B-2	Sequence 2, Appli
12	2.883.5	83.0	842	4	US-10-190-305A-2	Sequence 2, Appli
13	2.883.5	83.0	842	5	US-10-976-619-2	Sequence 2, Appli
14	2.883.5	83.0	847	3	US-09-476-242-2	Sequence 2, Appli
15	2.852	82.1	850	3	US-09-966-931-28	Sequence 28, Appli
16	2.852	82.1	850	4	US-10-459-121-28	Sequence 28, Appli
17	2.827.5	81.4	643	4	US-10-032-162-13	Sequence 13, Appli
18	2.827.5	81.4	643	5	US-10-780-993-13	Sequence 13, Appli
19	2.809.5	80.9	856	3	US-09-476-242-1	Sequence 1, Appli
20	2.809.5	80.9	856	5	US-10-891-125-19	Sequence 19, Appli
21	2.809.5	80.9	857	3	US-09-966-931-30	Sequence 30, Appli
22	2.809.5	80.9	857	4	US-10-459-121-30	Sequence 1, Appli
23	2.807	80.8	848	5	US-10-844-558-1	Sequence 1, Appli
24	2.806.5	80.8	863	5	US-10-634-165-11	Sequence 11, Appli
25	2.795.5	80.5	856	4	US-10-196-515-11	Sequence 11, Appli
26	2.795.5	80.5	856	6	US-11-048-554-11	Sequence 11, Appli
27	2.795	80.5	861	4	US-10-026-741-103	Sequence 103, App

ALIGNMENTS

RESULT 1
 US-09-938-406-1
 ; Sequence 1, Application US/09338406
 ; Patent No. US20020155120A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Vancoll, Thomas B
 ; BIRX, Deborah
 ; TITLE OF INVENTION: PROTEIN AND PEPTIDE VACCINES FOR INDUCING MUCOSAL IMMUNITY
 ; TITLE OF INVENTION: INDUCING MUCOSAL IMMUNITY
 ; FILE REFERENCE: 40646-2002.10
 ; CURRENT APPLICATION NUMBER: US/09/938,406
 ; CURRENT FILING DATE: 2001-08-21
 ; PRIORITY APPLICATION NUMBER: US 09/214,701
 ; PRIOR FILING DATE: 1999-09-30
 ; PRIORITY APPLICATION NUMBER: PCT/US 97/12253
 ; SEQ ID NO 1
 ; LENGTH: 868
 ; TYPE: PRT
 ; ORGANISM: Virus HIV-1
 ; US-09-938-406-1

Query Match Best Local Similarity 100.0% ; Score 3474; DB 3; Length 868;
 Matches 649; Conservative 0; Mismatches 0; Gaps 0;

Query Match Best Local Similarity 100.0% ; Score 3474; DB 3; Length 868;
 Matches 649; Conservative 0; Mismatches 0; Gaps 0;

QY 1 ANLWVTVYGYPVWKAEATTFLCASDATAVDTPEAHNVATHACYPTNPNPQEYVLYNTVE LENGTH 60
 Db 33 ANLWVTVYGYPVWKAEATTFLCASDATAVDTPEAHNVATHACYPTNPNPQEYVLYNTVE LENGTH 92

QY 1 ANLWVTVYGYPVWKAEATTFLCASDATAVDTPEAHNVATHACYPTNPNPQEYVLYNTVE LENGTH 61 NFMWKMNNVMEQHEDISLWDQSLKPCVKLPCLCVTNCNTDNTNTNTTELSIVVV LENGTH 120
 Db 93 NFMWKMNNVMEQHEDISLWDQSLKPCVKLPCLCVTNCNTDNTNTNTTELSIVVV LENGTH 152

QY 121 EQRGKEMCNSFNTTSIRDKVOREYALFYKLDEPIDDNKNTNTKYRLINCNTSYI LENGTH 180
 Db 153 EQRGKEMCNSFNTTSIRDKVOREYALFYKLDEPIDDNKNTNTKYRLINCNTSYI LENGTH 212

QY 181 TOACPKVSPEPHYCPTGPAFKLNDKKGFTGPCTNVSSTQCTHGIRPVVSSTQIL LENGTH 240
 Db 213 TOACPKVSPEPHYCPTGPAFKLNDKKGFTGPCTNVSSTQCTHGIRPVVSSTQIL LENGTH 272

QY 241 NGSLAEEVVIRESNPFTNNAKTIVQLNSVEINCTRPMNHTRKVTLGPGRVWTTGBI LENGTH 300
 Db 273 NGSLAEEVVIRESNPFTNNAKTIVQLNSVEINCTRPMNHTRKVTLGPGRVWTTGBI LENGTH 332

Qy	301	LGNRQAHNISRAQWNTLQQIATTIREQFGNKTIATQNSGGDPETIVMHSNCGBFP	360	
Db	333	LGNRQAHNISRAQWNTLQQIATTIREQFGNKTIATQNSGGDPETIVMHSNCGBFP	392	
Qy	361	YCNSTQLFNSAANVTSNGTWSVTRKQDITLPCRIKQIINRQVOVGKAMYALPKG	420	
Db	393	YCNSTQLFNSAANVTSNGTWSVTRKQDITLPCRIKQIINRQVOVGKAMYALPKG	452	
Qy	421	LIRCSSNTGLLTRDGGENOTEIIFRGGDMRDWRSELKYKVVKIEPLGVAPTKA	480	
Db	453	LIRCSSNTGLLTRDGGENOTEIIFRGGDMRDWRSELKYKVVKIEPLGVAPTKA	512	
Qy	481	KRIVVQREKAVGMFLGIGAGSTMAGTSMALTVQAROLLSGIVQQQNLLRAIK	540	
Db	513	KRIVVQREKAVGMFLGIGAGSTMAGTSMALTVQAROLLSGIVQQQNLLRAIK	572	
Qy	541	AQHHLQLTWKGIKOLOARIALLAVERYLKDQQLIGFWSGSKLUJCTTAYPWNSWSNCTLD	600	
Db	573	AQHHLQLTWKGIKOLOARIALLAVERYLKDQQLIGFWSGSKLUJCTTAYPWNSWSNCTLD	632	
Qy	601	QIANNMTMNEWDRIDNYTHLYTLIERSQNQEQKNOELLQDKWASL	649	
Db	633	QIANNMTMNEWDRIDNYTHLYTLIERSQNQEQKNOELLQDKWASL	681	
RESULT 2				
	US-10-780-507-51	Sequence 51, Application US/10780507		
		Publication No. US20050137387A1		
		GENERAL INFORMATION:		
		; APPLICANT: MULLINS, James I.		
		; APPLICANT: RODRIGO, Allen G.		
		; APPLICANT: LEARN, Gerald H.		
		; APPLICANT: LI, Fusheng		
		; APPLICANT: NICKLE, David C.		
		; APPLICANT: JENSEN, Mark A.		
		TITLE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPO		
		FILE REFERENCE: 16336-001320UT		
		CURRENT APPLICATION NUMBER: US/10/780,507		
		CURRENT FILING DATE: 2004-02-17		
		PRIOR APPLICATION NUMBER: US/10/204,204		
		PRIOR FILING DATE: 2001-02-16		
		PRIOR APPLICATION NUMBER: PCT/US01/05288		
		PRIOR FILING DATE: 2001-02-16		
		PRIOR APPLICATION NUMBER: US/60/183,659		
		PRIOR FILING DATE: 2000-02-18		
		PRIOR APPLICATION NUMBER: US/60/447,586		
		PRIOR FILING DATE: 2003-02-14		
		NUMBER OF SEQ ID NOS: 125		
		SOFTWARE: PatentIn version 3.1		
		SEQ ID NO 51		
		LENGTH: 862		
		TYPE: PRT		
		ORGANISM: Artificial sequence		
		FEATURE:		
		OTHER INFORMATION: Least squares and minimum of means center of tree reconstruction		
		OTHER INFORMATION: of clade B gp 160 protein sequence		
	US-10-780-507-51			
Query Match	86.0%	Score 2987; DB 5; Length 862;		
Best Local Similarity	86.6%	Pred. No. 1.e-227;		
Matches	563;	Conservative 31; Mismatches 6;		
Qy	3	LWTTVYYGPVWKEATTTLFCASDAKAYDTAEHNWATHACVPTNPNIQEYVLENTEFN	62	
	33	LWTTVYYGPVWKEATTTLFCASDAKAYDTAEHNWATHACVPTNPNIQEYVLENTEFN	92	
Db	63	NWYKNNNNYQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNTNTNTTELSIIIVVWEQ	122	
Qy	93	NWYKNNNNYQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLN-KNATNTSSS---GEM	147	
Db	123	RGKGENMCNFNITTSIRDVKOREYALFYKLDVEPIDDNNNTNTNNNTNNNTNNNTTSITC	182	
Qy	93	NWYKNNNNYQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLN-KNATNTSSS---GEM	152	

RESULT 4
US-10-441-949-2
; Sequence 2, Application US/10441949
; GENERAL INFORMATION:
; APPLICANT: Mullins, James I.
; TITLE OF INVENTION: ANCESTRAL VIRUSES AND VACCINES
; FILE REFERENCE: 08987-012001
; CURRENT APPLICATION NUMBER: US/10/441,949
; CURRENT FILING DATE: 2003-05-19
; PRIORITY APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2001-02-16
; PRIORITY APPLICATION NUMBER: US 60/183,659
; PRIORITY FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Artificially generated peptide
; US-10-441-949-2
; Query Match 85.7%; Score 2977.5; DB 4; Length 883;
; Best Local Similarity 84.7%; Pred. No. 6.5e-227; Mismatches 27; Indels 54; Gaps 6;
; Matches 564; Conservative 33; Gapopen 14
; 3 LWVTVYVGVPWKCAATTTCASDAKAYTDEAHNVWATHACVPTNPNPQEVLLENVTNF 62

QY 123 RG-----KGEMRNCSPNITTSIRDKVQREYALFYKLIDVEPEID-DNKNTNNNTKYRLIN 174
Db 153 SGGTMEGIGKEIKNCSFNVTTTSIRDKMREYALFYKLQVLPIDNDNNNTNTSYRLIN 212
Qy 175 CNTSVITQACPYSFEPIDPHCPTGPAFLKCNDKKGNGTGPCTNNUSTVQCTHGIRVV 234
Db 213 CNTSVITQACPYSFEPIDPHCPTGPAFLKCNDKKGNGTGPCTNNUSTVQCTHGIRVV 272
Qy 235 STOLLINGSLAEEVVIRSNFTNAAKTTIVQLNSVETCTRNHHTRKRVLTGPGRWV 294
Db 273 STOLLINGSLAEEVVIRSNFTNAAKTTIVQLNSVETCTRNHHTRKRVLTGPGRWV 332
Qy 295 YTTCGILGHNTROAHCNISRAQWNTLQQATTLRBQEQGNK-TIAFNQSSGDPPEIVHQS 352
Db 333 YATGKLGIDTRQAHNLSPAKWNNTLKVQVTKREQFGNNTKTTVFNQSGGDPPEIVHQS 392
Qy 353 FNCGGEFFYCNSTOLFNSAWNNTSNGNTWSYTRKQ---DTGDIITLPCRIKQIINWQ 407
Db 393 FNCGGEFFYCNSTOLFNSWNTHF--NGTMGNNTSNNADDNDTTLPCRIKQIINWQ 450
Qy 408 VVGKAMYAUPIKGLIHCSSNITGLLTDDGGENQT---TEIFRGGDMRDNRWSELY 463
Db 451 EVGKAMYAPPISGQTRCSNITGLLTDDGGENNTDTEIFRGGDMRDNRWSELY 510
Qy 464 KYKVKVKEPLGVAPTKAKRVRVOREKRAVGMFLGIGAAGSTMGAASMMLTVQRQ 523
Db 511 KYKVKVKEPLGVAPTKAKRVRVOREKRAVGMFLGIGAAGSTMGAASMMLTVQRQ 570
Qy 524 LLSGIVQOQNLLRAIKAQHLLQLOLTWKGKOLORARIHAVERTYLKDQQLGPGCGKLI 583
Db 571 LLSGIVQOQNLLRAIKAQHLLQLOLTWKGKOLORARIHAVERTYLKDQQLGPGCGKLI 630
Qy 584 CTTAVPNASWSNCKLDQIWNMTWMEIREIDNYTHLYTLLIBESQNEQKQELQI 633
Db 631 CTTAVPNASWSNCKLDQIWNMTWMEIREIDNYTGLLYTLLIBESQNEQKQELLEL 690
Qy 644 DKWASL 649
Db 691 DKWASL 696

RESULT 5
US-10-780-507-2
; Sequence 2, Application US/10780507
; GENERAL INFORMATION:
; PUBLICATION NO. US20050137387A1
; GENERAL INFORMATION:
; APPLICANT: MULLINS, James I.
; APPLICANT: RODRIGO, Allen G.
; APPLICANT: LEARN, Gerald H.
; APPLICANT: LI, Fusheng
; APPLICANT: NICKLE, David C.
; APPLICANT: JENSEN, Mark A.
; TITLE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPOUNDS
; CURRENT APPLICATION NUMBER: US/10/780,507
; CURRENT FILING DATE: 2004-02-17
; PRIORITY APPLICATION NUMBER: US/10/204,204
; PRIORITY FILING DATE: 2001-02-16
; PRIORITY APPLICATION NUMBER: PCT/US01/05288
; PRIORITY FILING DATE: 2001-02-16
; PRIORITY APPLICATION NUMBER: US 60/183,659
; PRIORITY FILING DATE: 2000-02-18
; PRIORITY FILING DATE: 2000-02-18
; PRIORITY FILING DATE: 2003-02-14
; PRIORITY FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1

SEQ ID NO 2
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ancestral HIV-1 group M, subtype B, env sequence
US-10-780-507-2

Query Match Score 2977.5; DB 5; Length 883;
Best Local Similarity 84.7%; Pred. No. 6.5e-227; Indels 21; Gaps 6;
Matches 564; Conservative 27; Mismatches 54;

QY 3 LWVTVYYGYPVWKEATTTLFCASDAKAYTEAHNVWATHACVPTNPQDPEVLENTEP 62
Db 33 LWVTVYYGYPVWKEATTTLFCASDAKAYTEEVNVWATHACVPTDPNQDPEVLENTEP 92

QY 63 NMWKNNMVEQMHEDISLMDQSJKPCVKLPLCVTLNCPLDNTNTTELSLIVVWEQ 122
Db 93 NMWKNNMVEQMHEDISLMDQSJKPCVKLPLCVTLNCPLDNTNTTELSLIVVWEQ 152

QY 123 RG-----KGEMRNCSPNITTSIRDKYOREALFYKLDPEYID-DNKNTTNTKYRLIN 174
Db 153 SGGGTMEEGKGEIKNCSFNVITSIRDKOREALFYKLVLPVLNDNNNTNNNTSYRLIN 212

QY 175 CNTSVITOACPKVSSFEPIPHCPTGPFLIKCNCKENGTGPTCNVSTVQCTHGIRPV 234
Db 213 CNTSVITOACPKVSSFEPIPHCPTGPFLIKCNCKENGTGPTCNVSTVQCTHGIRPV 272

QY 235 STOLLINGSLAEEVVIRSENFTNNAKTTIVQLNSVENCTRPNHTRKRVTLGPRGVW 294
Db 273 STOLLINGSLAEEVVIRSENFTNNAKTTIVQLNESVENCTRPNNTRKSPIGPGRAL 332

QY 295 YTTEBILGNTROAHCNISRAQWNNTLQOJATTLEOFGNK-TIAFNOSSGDPEIYHMS 352
Db 333 YATGKIGDTRQAHCNLSRAKWNNTLKQIVTURQRQFQGNKTTIVFNSSGDPEIYHMS 392

QY 353 FNCGSEFFYFCNSTOLFSNNSAWNTSNGTWSVTRKOK----DTGDIITLPCRIQIQINWQ 407
Db 393 FNCGSEFFYFCNSTOLFSNNSAWNTSNGTWSVTRKOK----DTGDIITLPCRIQIQINWQ 450

QY 408 VVGKAMYAPIKGLIRCSNNTGILLTRGGENQ---TEFRPGGGDMRDNWRSLEY 463
Db 451 EVGKAMYAPIPSQJRCSSNNTGILLTRGGNNNTNTDTEFRPGGGDMRDNWRSLEY 510

QY 464 KYKVVKIEPLGVAPTKAKRVRVQREKRAVGMFLGFLGAAGSTMAGTSMALTYQARQ 523
Db 511 KYKVVKIEPLGVAPTKAKRVRVQREKRAVGMFLGFLGAAGSTMAGTSMALTYQARQ 570

QY 524 LLSGIVQQQNLLRAIKAQHQLQLTYNGIKOLQARLAVERYLKDQOLGFWGCSKLI 583
Db 571 LLSGIVQQQNLLRAIKAQHQLQLTYNGIKOLQARLAVERYLKDQOLGFWGCSKLI 630

QY 584 CTTAVPNNSWSNKTLDQIWNNTTWENDREIDNYTHLYTLLBEONQEQNQELQI 643
Db 631 CTTAVPNNSWSNKSLDKLWNNTTWEMEREIDNYTGLIYTLLBEONQEQNQELQI 690

QY 644 DKWASL 649
Db 691 DKWASL 696

RESULT 6
US-10-780-507-121
Sequence 121, Application US/10780507
Publication No. US20050137387A1
GENERAL INFORMATION:
; APPLICANT: MULLINS, James I.
; APPLICANT: RODRIGO, Allen G.
; APPLICANT: LEARN, Gerald H.
; APPLICANT: LI, Fusibeng
; APPLICANT: NICKLE, David C.
; APPLICANT: JENSEN, Mark A.
; TITLE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPOUNDS

; FILE REFERENCE: 16336-001320US
; CURRENT APPLICATION NUMBER: US/10/780,507
; PRIOR APPLICATION NUMBER: US 2004-02-17
; PRIOR FILING DATE: 2004-10/24/204
; PRIOR APPLICATION NUMBER: 2001-02-16
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/183,659
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 121
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Deduced ancestor env protein sequence
; OTHER INFORMATION: US-10-780-507-121

Query Match Score 2977.5; DB 5; Length 883;
Best Local Similarity 84.7%; Pred. No. 6.5e-227;
Matches 564; Conservative 27; Mismatches 54;
Indels 21; Gaps 6;

QY 3 LWVTVYYGYPVWKEATTTLFCASDAKAYTEAHNVWATHACVPTNPQEVLENTEP 62
Db 33 LWVTVYYGYPVWKEATTTLFCASDAKAYTEEVNVWATHACVPTDPNQEVLENTEP 92

QY 63 NMWKNNMVEQMHEDISLMDQSJKPCVKLPLCVTLNCPLDNTNTTELSLIVVWEQ 122
Db 93 NMWKNNMVEQMHEDISLMDQSJKPCVKLPLCVTLNCPLDNTNTTELSLIVVWEQ 152

QY 123 RG-----KGEMRNCSPNITTSIRDKYOREALFYKLDPEYID-DNKNTTNTKYRLIN 174
Db 153 SGGGTMEEGKGEIKNCSFNVITSIRDKOREALFYKLVLPVLNDNNNTNNNTSYRLIN 212

QY 175 CNTSVITOACPKVSSFEPIPHCPTGPFLIKCNCKENGTGPTCNVSTVQCTHGIRPV 234
Db 213 CNTSVITOACPKVSSFEPIPHCPTGPFLIKCNCKENGTGPTCNVSTVQCTHGIRPV 272

QY 235 STOLLINGSLAEEVVIRSENFTNNAKTTIVQLNSVENCTRPNHTRKRVTLGPRGVW 294
Db 273 STOLLINGSLAEEVVIRSENFTNNAKTTIVQLNESVENCTRPNNTRKSPIGPGRAL 332

QY 295 YTTEBILGNTROAHCNISRAQWNNTLQOJATTLEOFGNK-TIAFNOSSGDPEIYHMS 352
Db 333 YATGKIGDTRQAHCNLSRAKWNNTLKQIVTURQRQFQGNKTTIVFNSSGDPEIYHMS 392

QY 353 FNCGSEFFYFCNSTOLFSNNSAWNTSNGTWSVTRKOK----DTGDIITLPCRIQIQINWQ 407
Db 393 FNCGSEFFYFCNSTOLFSNNSAWNTSNGTWSVTRKOK----DTGDIITLPCRIQIQINWQ 450

QY 408 VVGKAMYAPIKGLIRCSNNTGILLTRGGENQ---TEFRPGGGDMRDNWRSLEY 463
Db 451 EVGKAMYAPIPSQJRCSSNNTGILLTRGGNNNTNTDTEFRPGGGDMRDNWRSLEY 510

QY 464 KYKVVKIEPLGVAPTKAKRVRVQREKRAVGMFLGFLGAAGSTMAGTSMALTYQARQ 523
Db 511 KYKVVKIEPLGVAPTKAKRVRVQREKRAVGMFLGFLGAAGSTMAGTSMALTYQARQ 570

QY 524 LLSGIVQQQNLLRAIKAQHQLQLTYNGIKOLQARLAVERYLKDQOLGFWGCSKLI 583
Db 571 LLSGIVQQQNLLRAIKAQHQLQLTYNGIKOLQARLAVERYLKDQOLGFWGCSKLI 630

QY 584 CTTAVPNNSWSNKTLDQIWNNTTWENDREIDNYTHLYTLLBEONQEQNQELQI 643
Db 631 CTTAVPNNSWSNKSLDKLWNNTTWEMEREIDNYTGLIYTLLBEONQEQNQELQI 690

QY 644 DKWASL 649
Db 691 DKWASL 696

RESULT 6
US-10-780-507-121
Sequence 121, Application US/10780507
Publication No. US20050137387A1
GENERAL INFORMATION:
; APPLICANT: MULLINS, James I.
; APPLICANT: RODRIGO, Allen G.
; APPLICANT: LEARN, Gerald H.
; APPLICANT: LI, Fusibeng
; APPLICANT: NICKLE, David C.
; APPLICANT: JENSEN, Mark A.
; TITLE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPOUNDS

; FILE REFERENCE: 16336-001320US
; CURRENT APPLICATION NUMBER: US/10/780,507
; PRIOR APPLICATION NUMBER: US 2004-02-17
; PRIOR FILING DATE: 2004-10/24/204
; PRIOR APPLICATION NUMBER: 2001-02-16
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/183,659
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 121
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Deduced ancestor env protein sequence
; OTHER INFORMATION: US-10-780-507-121

Query Match Score 2977.5; DB 5; Length 883;
Best Local Similarity 84.7%; Pred. No. 6.5e-227;
Matches 564; Conservative 27; Mismatches 54;
Indels 21; Gaps 6;

QY 3 LWVTVYYGYPVWKEATTTLFCASDAKAYTEAHNVWATHACVPTNPQEVLENTEP 62
Db 33 LWVTVYYGYPVWKEATTTLFCASDAKAYTEEVNVWATHACVPTDPNQEVLENTEP 92

QY 63 NMWKNNMVEQMHEDISLMDQSJKPCVKLPLCVTLNCPLDNTNTTELSLIVVWEQ 122
Db 93 NMWKNNMVEQMHEDISLMDQSJKPCVKLPLCVTLNCPLDNTNTTELSLIVVWEQ 152

QY 123 RG-----KGEMRNCSPNITTSIRDKYOREALFYKLDPEYID-DNKNTTNTKYRLIN 174
Db 153 SGGGTMEEGKGEIKNCSFNVITSIRDKOREALFYKLVLPVLNDNNNTNNNTSYRLIN 212

QY 175 CNTSVITOACPKVSSFEPIPHCPTGPFLIKCNCKENGTGPTCNVSTVQCTHGIRPV 234
Db 213 CNTSVITOACPKVSSFEPIPHCPTGPFLIKCNCKENGTGPTCNVSTVQCTHGIRPV 272

QY 235 STOLLINGSLAEEVVIRSENFTNNAKTTIVQLNSVENCTRPNHTRKRVTLGPRGVW 294
Db 273 STOLLINGSLAEEVVIRSENFTNNAKTTIVQLNESVENCTRPNNTRKSPIGPGRAL 332

QY 295 YTTEBILGNTROAHCNISRAQWNNTLQOJATTLEOFGNK-TIAFNOSSGDPEIYHMS 352
Db 333 YATGKIGDTRQAHCNLSRAKWNNTLKQIVTURQRQFQGNKTTIVFNSSGDPEIYHMS 392

QY 353 FNCGSEFFYFCNSTOLFSNNSAWNTSNGTWSVTRKOK----DTGDIITLPCRIQIQINWQ 407
Db 393 FNCGSEFFYFCNSTOLFSNNSAWNTSNGTWSVTRKOK----DTGDIITLPCRIQIQINWQ 450

QY 408 VVGKAMYAPIKGLIRCSNNTGILLTRGGENQ---TEFRPGGGDMRDNWRSLEY 463
Db 451 EVGKAMYAPIPSQJRCSSNNTGILLTRGGNNNTNTDTEFRPGGGDMRDNWRSLEY 510

QY 464 KYKVVKIEPLGVAPTKAKRVRVQREKRAVGMFLGFLGAAGSTMAGTSMALTYQARQ 523
Db 511 KYKVVKIEPLGVAPTKAKRVRVQREKRAVGMFLGFLGAAGSTMAGTSMALTYQARQ 570

QY 524 LLSGIVQQQNLLRAIKAQHQLQLTYNGIKOLQARLAVERYLKDQOLGFWGCSKLI 583
Db 571 LLSGIVQQQNLLRAIKAQHQLQLTYNGIKOLQARLAVERYLKDQOLGFWGCSKLI 630

QY 584 CTTAVPNNSWSNKTLDQIWNNTTWENDREIDNYTHLYTLLBEONQEQNQELQI 643
Db 631 CTTAVPNNSWSNKSLDKLWNNTTWEMEREIDNYTGLIYTLLBEONQEQNQELQI 690

QY 644 DKWASL 649
Db 691 DKWASL 696

RESULT 7
US-10-780-507-50
Sequence 50, Application US/10780507
Publication No. US20050137387A1
GENERAL INFORMATION:
APPLICANT: MULLINS, James I.
APPLICANT: RODRIGO, Allen G.
APPLICANT: LEARN, Gerald H.
APPLICANT: LI, Fusheng
APPLICANT: NICKLE, David C.
APPLICANT: JENSEN, Mark A.

TITLE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPOUNDS

FILE REFERENCE: 16336-001320US

CURRENT APPLICATION NUMBER: US/10/780,507

CURRENT FILING DATE: 2004-02-17

PRIOR APPLICATION NUMBER: US/10/204,204

PRIOR FILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: PCT/US01/05288

PRIOR FILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: US 60/183,659

PRIOR FILING DATE: 2000-02-18

PRIOR APPLICATION NUMBER: US 60/447,586

PRIOR FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 125

SOFTWARE: Patentin version 3.1

SEQ ID NO 50

LENGTH: 862

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Most recent common ancestor reconstruction of clade B gp 160 protein

OTHER INFORMATION: ein sequence

US-10-780-507-50

Query Match 84.9%; Score 2949; DB 5; Length 862;
Best Local Similarity 85.6%; Pred. No. 1.1e-24;
Matches 557; Conservative 32; Mismatches 52; Indels 10; Gaps 6;

Db 2 NLWVTVYYGVWVKREATTLFCASDAKAYTKEATTLECASDAKAYTKEATTLECASDAKAYTKEEVNWATHACVTPDNPQEVVLENTE 61
Db 32 NLWVTVYYGVWVKREATTLFCASDAKAYTKEATTLECASDAKAYTKEEVNWATHACVTPDNPQEVVLENTE 91

Qy 62 FNMWKDNMVEQMHEDISLWDQSLKPCVNLTKPLCYTLNCTDLNTNTNTTELSTIIVME 121
Db 92 FNMWKDNMVEQMHEDISLWDQSLKPCVNLTKPLCYTLNCTDLNTNTNTTELSTIIVME 146

Qy 122 QRGKGMRCNSFNITTSIRDKVOREYALFYKLVDPIIDNKNTINTRKLINCNTSVT 181
Db 147 TMEKGEMKNCNSFNITTSIRDKVOREYALFYKLVDPIIDNNSSNNTNRLINCNTSVT 206

Qy 182 QACPYSFEPPIHYCTPGLFLCKNDKFENGTCPTVNSTVQCTHGRPVVSTQLLIN 241
Db 207 QACPYSFEPPIHYCTPAGPAFKLCKNDKFENGTCPTVNSTVQCTHGRPVVSTQLLIN 266

Qy 242 GSLABEBVIRSENFTNNAKTIYOLVNSYBENCTRPNNHTKRKVTLGPRVWTTGEL 301
Db 267 GSLABEBVIRSENFTNNAKTIYOLVNSYBENCTRPNNHTKRKVTLGPRVWTTGEL 326

Qy 302 GMNROHCNISRAQNNNTLQIAQTILREQG-NKTIATFNOSSGGDPETIMHSFNGGPF 360
Db 327 GDIRQHCNISRAQNNNTLQIVVTKREOFENNCTIVNFSGGDPETIMHSFNGGPF 386

Qy 361 YCNSTOLNSAWNNTSNTVSUTKRDGTIDITLPCRGMDMRDWRSELSELYKVKYKIEPLGVAPT 420
Db 387 YCNTOFLNSWNST-BEGSKNTTGSNTNGETITLPCRGMDMRDWRSELSELYKVKYKIEPLGVAPT 445

Qy 421 LIRCSSNTGHLITRDGGGENOT-TEIIPRGGGDMRDWRSELSELYKVKYKIEPLGVAPT 478
Db 446 QIKCSSNTGHLITRD-GGENSTNETEIFFREGGGDMRDWRSELSELYKVKYKIEPLGVAPT 504

Qy 479 KAKRRVYQREKRAVGMGLGMLGFLGIGAAGSTMGATSMALLTQAROLLSIVQQNNLLRA 538

RESULT 8
US-10-093-953A-29
Sequence 29, Application US/10093953A
Publication No. US20040105871A1
GENERAL INFORMATION:
APPLICANT: Robinson, Harriet L.
APPLICANT: Smith, James M.
APPLICANT: Hua, Jian
APPLICANT: Mose, Bernard
APPLICANT: Amara, Rama
APPLICANT: Wyatt, Linda
APPLICANT: Earl, Patricia
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENERATING
TITLE OF INVENTION: AN IMMUNE RESPONSE
FILE REFERENCE: 12804-0050102
CURRENT APPLICATION NUMBER: US/10/093,953A
CURRENT FILING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: US 60/186,364
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/251,083
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/798,675
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: PCT/US01/06795
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/324,845
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 09/798,675
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 852
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: protein encoded by construct of vaccine vector
OTHER INFORMATION: JS2 and insert JS2 expressing clade HIV-1 VL
US-10-093-953A-29

Query Match 83.4%; Score 2896.5; DB 4; Length 852;
Best Local Similarity 83.6%; Pred. No. 1.6e-220;
Matches 544; Conservative 40; Mismatches 48; Indels 19; Gaps 6;

Qy 2 NLWVTVYYGVWVKREATTLFCASDAKAYTDEAHNWATHACVTPDNPQEVVLENTE 61
Db 32 NLWVTVYYGVWVKREATTLFCASDAKAYTDEAHNWATHACVTPDNPQEVVLENTE 91

Qy 62 FNMWKDNMVEQMHEDISLWDQSLKPCVNLTKPLCYTLNCTDLNTNTNTTELSTIIVME 121
Db 92 FNMWKDNMVEQMHEDISLWDQSLKPCVNLTKPLCYTLNCTDLNTNTNTTELSTIIVME 146

Qy 122 QRGKGMRCNSFNITTSIRDKVOREYALFYKLVDPIIDNKNTINTRKLINCNTSVT 181
Db 147 TMEKGEMKNCNSFNITTSIRDKVOREYALFYKLVDPIIDNNSSNNTNRLINCNTSVT 206

Qy 182 QACPYSFEPPIHYCTPGLFLCKNDKFENGTCPTVNSTVQCTHGRPVVSTQLLIN 241
Db 207 QACPYSFEPPIHYCTPAGPAFKLCKNDKFENGTCPTVNSTVQCTHGRPVVSTQLLIN 266

Qy 242 GSLABEBVIRSENFTNNAKTIYOLVNSYBENCTRPNNHTKRKVTLGPRVWTTGEL 301
Db 267 GSLABEBVIRSENFTNNAKTIYOLVNSYBENCTRPNNHTKRKVTLGPRVWTTGEL 326

Qy 302 GMNROHCNISRAQNNNTLQIAQTILREQG-NKTIATFNOSSGGDPETIMHSFNGGPF 360
Db 327 GDIRQHCNISRAQNNNTLQIVVTKREOFENNCTIVNFSGGDPETIMHSFNGGPF 386

Qy 361 YCNSTOLNSAWNNTSNTVSUTKRDGTIDITLPCRGMDMRDWRSELSELYKVKYKIEPLGVAPT 420
Db 387 YCNTOFLNSWNST-BEGSKNTTGSNTNGETITLPCRGMDMRDWRSELSELYKVKYKIEPLGVAPT 445

Qy 421 LIRCSSNTGHLITRDGGGENOT-TEIIPRGGGDMRDWRSELSELYKVKYKIEPLGVAPT 478
Db 446 QIKCSSNTGHLITRD-GGENSTNETEIFFREGGGDMRDWRSELSELYKVKYKIEPLGVAPT 504

Qy 479 KAKRRVYQREKRAVGMGLGMLGFLGIGAAGSTMGATSMALLTQAROLLSIVQQNNLLRA 538

Db 257 SLABEGVIRSENFTDNAKTTIVQLKESVBINCTRPNINTRKSITIGPGRAYATGDIIG 316
 Qy 303 NIROAHCNISRAQWNTLQQIATTIREFQFNKTIAFNOSSGGDPETVMMSPNCGGEFFYC 362
 Db 311 DIROAHCNISGEKWNTLQQIATTIREFQFNKTIAFNOSSGGDPETVMMSPNCGGEFFYC 376
 Db 317 NSTQLFNSAVENT----SNGTWSUTRKQDGTGDLITLPCRQKQINRQVVKMYALP 417
 Qy 363 NSTQLFNSAVENT----SNGTWSUTRKQDGTGDLITLPCRQKQINRQVVKMYALP 417
 Db 377 NSTQLFNSAVENT----ITLPCKRQKQINRQEVGKMYAPP 423
 Db 377 NSTQLFNSAVENT----ITLPCKRQKQINRQEVGKMYAPP 423
 Qy 418 IKGLIIRCSSNITGLLTDQGGE-NOTTEIIFRGCGDMRDNRWSELYKVKVKEPLGVA 476
 Db 424 IRGQIRCSSNITGLLTDQGKEISNTTEIIFRGCGDMRDNRWSELYKVKVKEPLGVA 483
 Qy 424 IRGQIRCSSNITGLLTDQGKEISNTTEIIFRGCGDMRDNRWSELYKVKVKEPLGVA 483
 Qy 477 PTKAKERVYOREKRAVGMGLGAMFLGPIAGAGSTMGATSMALTYQARQLSGIVOCQNNIL 536
 Db 484 PTKAQHLLQLTWGIKOLQARILAVERYLKQDQQLGFNGCSKLICITAVPNASWN 542
 Qy 537 RAIKAQHLLQLTWGIKOLQARILAVERYLKQDQQLGFNGCSKLICITAVPNASWN 596
 Db 543 RAIKAQHLLQLTWGIKOLQARILAVERYLKQDQQLGFNGCSKLICITAVPNASWN 602
 Qy 597 KTLDDQIWNNTMWEIDNYTHLYTIBESONQEBQNQELLDKWL 649
 Db 603 KSLDQIWNNTMWEIDNYTHLYTIBESONQEBQNQELLDKWL 655

RESULT 12
 US-10-190-305A-2
 ; Sequence 2, Application US/10190305A
 ; Publication No. US20030198621A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZUR MEGEDE, Jan
 ; APPLICANT: BARNETT, Susan
 ; APPLICANT: LIAN, Ying
 ; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B AND/OR
 ; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
 ; FILE REFERENCE: 2302-18702 / 18702-002
 ; CURRENT APPLICATION NUMBER: US/10/190,305A
 ; CURRENT FILING DATE: 2002-07-05
 ; NUMBER OF SEQ ID NOS: 93
 ; SEQ ID NO 2
 ; LENGTH: 842
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: SF162
 US-10-190-305A-2

Query Match 83.0%; Score 2883.5; DB 4; Length 842;
 Best Local Similarity 83.3%; Pred. No. 1.7e-219; Indels 31; Gaps 7;
 Matches 544; Conservative 40; Mismatches 38; Indels 31; Gaps 7;

Qy 3 LWVTVYYGVPWKEATTTLFCASDAKAYDTPEAHNTWATHACVTPNPQEVLNTENF 62
 Db 38 LWVTVYYGVPWKEATTTLFCASDAKAYDTPEAHNTWATHACVTPNPQEVLNTENF 87
 Qy 63 NMWKNNMVEQHEDITSLWDQSLKPCVKLPLCWTLNCTDLNTNTNTTELSTLIVVMEQ 122
 Db 88 NMWKNNMVEQHEDITSLWDQSLKPCVKLPLCWTLNCTDLNTNTNTTELSTLIVVMEQ 141
 Qy 123 RGKGEMRNCSFNITSIRDKVOREYALFYKLDVEPIDDNKNTNTKYRLINCNTSVITQ 182
 Db 142 MDRGEIKNCSPKVYTTSRKMKOKEYALFYKLDVVPIDN----DNTSYKLINCNTSVITQ 196
 Qy 183 ACPKVSFEPIPYPHCPTGPALLKNDKCKNGTGTCTNIVSTVQCTHGIKPVYSTOLLING 242
 Db 197 ACPKVSFEPIPYPHCAPAGPAKLCFKLNDKCKNGSFCNTVSTVQCTHGIKPVYSTOLLING 256
 Qy 243 SLAEEVVIRSENFTDNAKTTIVQLKESVBINCTRPNINTRKSITIGPGRAYATGDIIG 302
 Db 257 SLAEEGVVIRSENFTDNAKTTIVQLKESVBINCTRPNINTRKSITIGPGRAYATGDIIG 316

RESULT 15
 US-09-966-931-28
 ; Publication No. US/09666931
 ; GENERAL INFORMATION:
 ; APPLICANT: Berman, Phillip W.
 ; Nakamura, Gerald R.
 ; TITLE OF INVENTION: HIV Envelope Polypeptides
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McCurchen, Doyle, Brown & Emersen, LLP
 ; STREET: 3 Embarcadero Center
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/966,931
 ; FILING DATE: 27-Sep-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 09/492,739
 ; FILING DATE: 2000-01-27
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Halliday, Emily
 ; REGISTRATION NUMBER: 38903
 ; REFERENCE/DOCKET NUMBER: 14918-704
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-793-2000
 ; TELEFAX: 415-393-2286
 ; TELEX: <Unknown>
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 850 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Qy 363 NSTQLFNSANNV-----SNGTWSVTRKQKDGTIDITPCRIKOLINRVOVGRAMYALP 417
 Db 382 NSTQLFNSNTWNTIGPANTNG-----TLPCKRIKQJINRQEVGRAMYAPP 428
 Qy 418 IKGGLRCSNITGLLITRDGGCB-NOTTEIIRPQGGDMRDNRWSELYKVKVKTBPLGVA 476
 Db 429 IRGQIROSNSNITGLLITRDGGEBISNTTEIIRPQGGDMRDNRWSELYKVKVKTBPLGVA 488
 Qy 477 PTKAQKRVVQREKRAVGMIGANFLGAACSTMGATSMALTVQRQLSLCIVQQNNLL 536
 Db 489 PTKAQKRVVQREKRAV-TLGAMFLGFTGAASSTMGARSLLTVQRQLSLCIVQQNNLL 547
 Qy 537 RAIKAQHQLLTWKGKIKOLOQARILAVERYLKDQOLQFLGFCGSKLICITAVPNASWN 596
 Db 548 RAIEAQHQLLTWKGKIKOLOQARILAVERYLKDQOLQFLGFCGSKLICITAVPNASWN 607
 Qy 597 KTLDDQINWNMTWMEDREIDNYTHLTYLTIESONQEKNQELLDKVASL 649
 Db 608 KSLDDQINWNMTWMEDREIDNYTHLTYLTIESONQEKNQELLDKVASL 660

Db 33 LWVTTYYGYPVWKEATTILFCASDAKAYDTEVHNWATHACVPTDPNPQEIGLENVTENF 92
 Qy 63 NMWKDNMVEQMHEDISLWDOSLKECVKLTPLCVTLNCIDLNNTNTNTBLSIVVWEQ 122
 Db 93 NMWKDNMVEQMHEDISLWDOSLKECVKLTPLCVTLNCIDL-KNATNTSSSS---WGR 146
 Qy 123 RGKGMNRCNSNITTSIRDVKVREYALFYKLIDVERBIDDNRNTNTTKYLNCHNTSVITQ 182
 Db 147 MERGEIKNCSENVTSISTRDKMKNEVALFKLVDVFDN----DNTSYRLISCNNTSVITQ 201
 Qy 183 ACPKTSFEPITHCTPTGFALLKNDKCKENGTCFTNSTVQCTGIREPVVSTOLLING 242
 Db 202 ACPKTSFEPITHCAPAGFAILCRDKCEKENGTCFTNSTVQCTGIREPVVSTOLLING 261
 Qy 243 SIAEEBVVIRSENFTNNAACTIVIQLQNLNSVBEINCPRNNHTKRKVTLGPRWVTTGEIG 302
 Db 262 SIAEEBVVIRSENFDNAACTIVIQLQNLNSVBEINCPRNNTRSRTHGSPRAYATEIG 321
 Qy 303 NIROQHCNTSRAQNNNTLQOJATTLEQFNQNKTAFNQSSGGDPPIVWHISFNCGEFFYC 362
 Db 322 DIRQHCNLSSTRKWNNTLQOJIVTKREHF-NKTFVNHSGGDPPIVWHISFNCGEFFYC 380
 Qy 363 NSTQLFNSAWNNTSNGTWSVTRKQKDGTIDITPCRIKOLINRVOVGRAMYALPFGKLI 422
 Db 381 NTTPFLNSTWNTY-TWNTEGENDTGRIINTLQCRIKOLINMVEGRAMYAPPRGQI 438
 Qy 423 RCSSNITGLLITRDGGGENOTTEFRPGGCDMRDNWRSLEYKVKVKIBPLGVAFTKAR 497
 Db 439 RCSSNITGLLITRD-GCNNTSET1FRPGGCDMRDNWRSLEYKVKVKIBPLGVAFTKAR 542
 Qy 483 RVVQREKRAVGMFLGFLGAACSTMGMATSMALTVQRQLSLGIVQQNNLLRAIKAQ 556
 Db 498 RVVQREKRAV-IGAVFLGPLGAACSTMGMASVTLVQRLLSLGIVQQNNLLRAIEA 556
 Qy 543 QHLIQLTWGSIKOLQARILAVERYLKDQOLQFLGFCGSKLICITAVPNASWNKTLQDQI 602
 Db 557 QHLIQLTWGSIKOLQARILAVERYLKDQOLQFLGFCGSKLICITAVPNASWNLSDKI 616
 Qy 603 WDNMTWMEDREIDNYTHLTYLTIESONQEKNQELLDKVASL 649
 Db 617 WDNMTWMEDREIDNYTSLIYSLIESONQEKNQELLDKVASL 663

Search completed: March 7, 2006, 17:56:38
 Job time : 2:12.547 secs

3 LWVTTYYGYPVWKEATTILFCASDAKAYDTEVHNWATHACVPTDPNPQEIGLENVTENF 62

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OM protein - protein search, using sw model

Run on: March 7, 2006, 17:53:05 ; Search time 24.8879 Seconds
 (without alignments)
 521.549 Million cell updates/sec

Title: US-09-938-406-1_COPY_33_681

Perfect score: 349

Sequence: 1 ANLWWTYYGYPVWKBEATT.....QNQEKENQQELQLDKWASL 649

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 135346 seqs, 20000420 residues

Total number of hits satisfying chosen parameters: 135346

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_New:
 1: /cgn2_6/prodata/1/pubpaas/US08_NEW_PUB_pep:
 2: /cgn2_6/prodata/1/pubpaas/US06_NEW_PUB_pep:
 3: /cgn2_6/prodata/1/pubpaas/US07_NEW_PUB_pep:
 4: /cgn2_6/prodata/1/pubpaas/US09_NEW_PUB_pep:
 5: /cgn2_6/prodata/1/pubpaas/US05_NEW_PUB_pep:
 6: /cgn2_6/prodata/1/pubpaas/US10_NEW_PUB_pep:
 7: /cgn2_6/prodata/1/pubpaas/US11_NEW_PUB_pep:
 8: /cgn2_6/prodata/1/pubpaas/US60_NEW_PUB_pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	2809.5	80.9	856	6	US-10-510-947-8	Sequence 8, Appli
2	2809.5	80.9	856	7	US-11-042-888-13	Sequence 13, Appli
3	2809.5	80.9	856	7	US-11-135-235-1	Sequence 1, Appli
4	2756.5	79.3	681	7	US-11-014-842A-25	Sequence 25, Appli
5	2756.5	79.3	869	7	US-11-014-842A-27	Sequence 27, Appli
6	2668.5	76.8	669	7	US-11-014-842A-29	Sequence 29, Appli
7	2668.5	76.8	851	7	US-11-014-842A-31	Sequence 31, Appli
8	2509.5	72.2	613	7	US-11-014-842A-33	Sequence 33, Appli
9	2509.5	72.2	801	7	US-11-014-842A-35	Sequence 35, Appli
10	2489	71.6	854	7	US-11-022-852-219	Sequence 219, Appli
11	2421.5	69.7	601	7	US-11-014-842A-37	Sequence 37, Appli
12	2421.5	69.7	789	7	US-11-014-842A-39	Sequence 39, Appli
13	1140	32.8	879	7	US-11-022-562-340	Sequence 340, Appli
14	1112.5	32.0	860	7	US-11-022-562-217	Sequence 217, Appli
15	1153	18.8	145	7	US-11-084-858-11	Sequence 11, Appli
16	511.5	14.7	379	7	US-11-116-203-3	Sequence 3, Appli
17	436.5	12.6	146	7	US-11-084-858-10	Sequence 10, Appli
18	330.5	9.5	220	7	US-11-151-598-1	Sequence 1, Appli
19	330.5	9.5	225	7	US-11-151-598-7	Sequence 7, Appli
20	330.5	9.5	225	7	US-11-151-598-8	Sequence 8, Appli
21	330.5	9.5	227	7	US-11-151-598-9	Sequence 9, Appli
22	330.5	9.5	267	7	US-11-151-598-2	Sequence 2, Appli
23	316	9.1	213	7	US-10-841-956A-19	Sequence 19, Appli
24	275	7.9	151	7	US-11-022-562-215	Sequence 215, Appli
25	265	7.6	102	6	US-10-841-956A-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1
 US-10-510-947-8
 Sequence 8, Application US10510947
 ; Publication No. US20050255123A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Trustees of the University of Pennsylvania
 ; APPLICANT: Wilson, James M.
 ; APPLICANT: Medina, Maria Fe C.
 ; APPLICANT: Kobinger, Gary
 ; TITLE OF INVENTION: Chimeric Ebola Virus Envelopes and Uses, Therefor
 ; FILE REFERENCE: UPN-Q2811FCFT
 ; CURRENT FILING DATE: 2004-10-28
 ; PRIOR APPLICATION NUMBER: US 60/376,480
 ; PRIORITY FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/385,704
 ; PRIORITY FILING DATE: 2002-06-04
 ; PRIOR APPLICATION NUMBER: US 60/427,752
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO: 8
 ; LENGTH: 856
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus type 1
 US-10-510-947-8

Query Match 80.9%; Score 2809.5; DB 6; Length 856;
 Best Local Similarity 80.6%; Pred. No. 4.6e-251;
 Matches 538; Conservative 38; Missmatches 56; Gaps 9;

Qy 3 LWVTTYYGPPWKEATTTCFCAASDAAKAYTEARNWATHACVPTPNPQEVBLENVNENF 62
 Db 34 LWVTTYYGPPWKEATTTCFCAASDAAKAYTEARNWATHACVPTPNPQEVBLENVNENF 93
 Qy 63 NMWKNINMVEQMHED1ISLMQDSLKPCVKLTPLCYTLNCITDLANTNTNTTELSTIIVVWEQ 122
 Db 94 NMWKNIDMVEQMHED1ISLMQDSLKPCVKLTPLCYSLKCTDL-KDINTNNSSGRMIME- 150
 Qy 123 RGKGFMRNCSEFNITSIRDKVQEYALFYKLQDVPEIDDNKNTNTKYRLINCNTSVTQ 182
 Db 151 --KGFIKNCSEFNITSIRDKVQEYAFFKLQDIPDN----DTTSYKLTSCTNSVTQ 203
 Qy 183 ACPRKSFEPPIPHCTPFGALLKNDKFENGSPCTINSTVOCHGIRPVVSTOLLNG 242
 Db 204 ACPRKSFEPPIPHCAGPAGEFAILKCNNTFNGTCPCTNSTVQCHGIRPVVSTOLLNG 263
 Qy 243 SLAEFBVIRSENFTNNAKTIVIOLANVSBNCRNNHTRKRVTL-GPGRWYTTGBI 300

Db	264 SLAEEEVVRSVNFTDNAKTIVQLNTSVEINCRPNNTRKRIRIQRGPRAFTIGI	323	Db	264 SLAEEEVVRSVNFTDNAKTIVQLNTSVEINCRPNNTRKRIRIQRGPRAFTIGI	323
Qy	301 LGNTROAHCNISRAQWNNTLQOIAATTLRQFG-NKTIATFNOSSGGDPRIVMHESFNCGGRF	359	Qy	301 LGNTROAHCNISRAQWNNTLQOIAATTLRQFG-NKTIATFNOSSGGDPRIVMHESFNCGGRF	359
Db	324 -GNNRQAHCNISRAQWNNTLQOIAATTLRQFG-NKTIATFNOSSGGDPRIVMHESFNCGGRF	382	Db	324 -GNNRQAHCNISRAQWNNTLQOIAATTLRQFG-NKTIATFNOSSGGDPRIVMHESFNCGGRF	382
Qy	360 FYCNSTOLFNSAVNNTSGTWSUTRKQKDGT-DITLPCRQIKOINNPROVKGAMYALP	418	Qy	360 FYCNSTOLFNSAVNNTSGTWSUTRKQKDGT-DITLPCRQIKOINNPROVKGAMYALP	418
Db	383 FYCNSTOLFNSAVNNTSGTWSUTRKQKDGT-DITLPCRQIKOINNPROVKGAMYALP	418	Db	383 FYCNSTOLFNSAVNNTSGTWSUTRKQKDGT-DITLPCRQIKOINNPROVKGAMYALP	418
Qy	419 KGLIRCSSNTIGLLTRDGGENOTEI.FRPGGDMRDNRWLSLYCKVVKLEPLGVAPT	478	Qy	419 KGLIRCSSNTIGLLTRDGGENOTEI.FRPGGDMRDNRWLSLYCKVVKLEPLGVAPT	478
Db	440 SGQIQCNSNTIGLLTRDGGNSNESE.FRGGGDMRDNRWLSLYCKVVKLEPLGVAPT	499	Db	440 SGQIQCNSNTIGLLTRDGGNSNESE.FRGGGDMRDNRWLSLYCKVVKLEPLGVAPT	499
Qy	479 KAKRVRVOREKRAVGMGLAMFLGFLGAGSTMGATSMALTYQAROLISGIYQOQNLLRA	538	Qy	479 KAKRVRVOREKRAVGMGLAMFLGFLGAGSTMGATSMALTYQAROLISGIYQOQNLLRA	538
Db	500 KAKRVRVOREKRAV-IGALFLGFLGAGSTMGAASTMILTVQAROLISGIYQOQNLLRA	558	Db	500 KAKRVRVOREKRAV-IGALFLGFLGAGSTMGAASTMILTVQAROLISGIYQOQNLLRA	558
Qy	539 IKAQHQLQLTWGKQOLQARIAYERLYKDQOLIGFWGGSKLICITAVPNASWSNKT	598	Qy	539 IKAQHQLQLTWGKQOLQARIAYERLYKDQOLIGFWGGSKLICITAVPNASWSNKT	598
Db	559 IEAQHQLQLTWGKQOLQARIAYERLYKDQOLIGFWGGSKLICITAVPNASWSNKT	618	Db	559 IEAQHQLQLTWGKQOLQARIAYERLYKDQOLIGFWGGSKLICITAVPNASWSNKT	618
Qy	599 LDQIWNNTMWDREIDNYTHLYTTLIESONQEQEKNQELLQLDKWL	649	Qy	599 LDQIWNNTMWDREIDNYTHLYTTLIESONQEQEKNQELLQLDKWL	649
Db	619 LEQIWNHTTWWEDREINNTSLHSLIESONQEQEKNQELLQLDKWL	669	Db	619 LEQIWNHTTWWEDREINNTSLHSLIESONQEQEKNQELLQLDKWL	669
RESULT 3					
US-11-135-235-1					
; Sequence 1, Application US/11135235					
; Publication No. US2006019395A1					
; GENERAL INFORMATION:					
; APPLICANT: Marasco, Wayne					
; TITLE OF INVENTION: Lentiviral Vectors and Uses Thereof					
; FILE REFERENCE: 20363-027					
; CURRENT APPLICATION NUMBER: US/11/135,235					
; CURRENT FILING DATE: 2005-05-23					
; PRIORITY APPLICATION NUMBER: 60/589,610					
; PRIOR FILING DATE: 2004-07-21					
; NUMBER OF SEQ ID NOS: 25					
; SOFTWARE: Patentin version 3.2					
; SEQ ID NO: 1					
; LENGTH: 856					
; TYPE: PRT					
; ORGANISM: Human immunodeficiency virus type 1					
; SEQ ID NO: 13					
; LENGTH: 856					
; TYPE: PRT					
; ORGANISM: Human immunodeficiency virus type 1					
US-11-042-988-13					
; Sequence 13, Application US/11042988					
; Publication No. US20050244818A1					
; GENERAL INFORMATION:					
; APPLICANT: SILICIANO, ROBERT					
; APPLICANT: ZHANG, HAILI					
; APPLICANT: ZHOU, YAN					
; TITLE OF INVENTION: SINGLE CELL ANALYSIS OF HIV REPLICATION CAPACITY AND					
; FILE REFERENCE: 62760 (71639)					
; CURRENT APPLICATION NUMBER: US/11/042,988					
; CURRENT FILING DATE: 2005-01-25					
; PRIOR APPLICATION NUMBER: 60/540,716					
; PRIOR FILING DATE: 2004-01-30					
; NUMBER OF SEQ ID NOS: 16					
; SOFTWARE: Patentin ver. 3.3					
; SEQ ID NO: 13					
; LENGTH: 856					
; TYPE: PRT					
; ORGANISM: Human immunodeficiency virus type 1					
US-11-042-988-13					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					
; Best Local Similarity 82.6%; Pred. No. 4.6e-251; Mismatches 56; Indels 19; Gaps 9;					
; Matches 538; Conservative 38; Mismatches 38; Indels 19; Gaps 9;					
; Query Match Score 2809 5; DB 7; Length 856;					

RESULT 4
 Sequence 25, Application US/11/014842A
 Publication No. US2006001386A1

GENERAL INFORMATION:

APPLICANT: TANGY, FREDERIC
 APPLICANT: LORIN, CLARISSA
 APPLICANT: MOLLET, LUCILE
 APPLICANT: DELBECQUE, FREDERIC
 TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES - USE FOR THE PREPARATION OF
 TITLE OF INVENTION: VACCINE COMPOSITIONS
 FILE REFERENCE: 2356-0093
 CURRENT APPLICATION NUMBER: US/11/014, 842A
 CURRENT FILING DATE: 2004-12-20
 PRIOR APPLICATION NUMBER: PCT/EP03/07146
 PRIOR FILING DATE: 2003-06-10
 PRIOR APPLICATION NUMBER: EP 02291550.8
 PRIOR FILING DATE: 2002-06-20
 NUMBER OF SEQ ID NOS: 43
 SOFTWARE: PatentIn Ver. 3.3
 SEQ ID NO: 25
 LENGTH: 681
 TYPE: PRT
 ORGANISM: Human immunodeficiency virus type 1
 US 11-014-842A-25

RESULT 5
 Sequence 27, Application US/11/014842A
 Publication No. US2006001386A1

GENERAL INFORMATION:

APPLICANT: TANGY, FREDERIC
 APPLICANT: LORIN, CLARISSA
 APPLICANT: MOLLET, LUCILE
 APPLICANT: DELBECQUE, FREDERIC
 TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPESS OF
 TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
 FILE REFERENCE: 2356-0093
 CURRENT APPLICATION NUMBER: US/11/014, 842A
 CURRENT FILING DATE: 2004-12-20
 PRIOR APPLICATION NUMBER: PCT/EP03/07146
 PRIOR FILING DATE: 2003-06-10
 PRIOR APPLICATION NUMBER: EP 02291550.8
 PRIOR FILING DATE: 2002-06-20
 NUMBER OF SEQ ID NOS: 43
 SOFTWARE: PatentIn Ver. 3.3
 SEQ ID NO: 27
 LENGTH: 869
 TYPE: PRT
 ORGANISM: Human immunodeficiency virus type 1
 US 11-014-842A-27

Query Match 79.3%; Score 2756.5; DB: 7; Length 681;
 Best Local Similarity 79.4%; Pred. No. 2.6e-246; Mismatches 60; Indels 21; Gaps 8;
 Matches 517; Conservative 1

Query 3 LWVTTYYGVPWREATTIPLCSDAKAYDTEAHNYWATHACVPTNPNEBVLENTEP
 Db 63 NMWKNNMVEQMHEDISLWDLSKPCVKLPLCUTLNCTDLN-TNTNTNTTELSTIVME 121
 Db 94 NMWKNNMVDQMHEDISLWDLSKPCVKLPLCUTLNCTNLNITNTNTNLSSS---WG 149
 Query 122 QRGKGMRSFNPNTTSIRDKVQEVALFKLDPIDNKNTNTKRLINGNTSVT 181
 Db 150 MMEEGPIKNSFYTTSIRDKVQEVALFKLDPIDNKNTNTKRLINGNTSVT 205
 Query 182 QACPVKSFPPIPHTCPGTFALLCNDKNTNTKRLINGNTSVT 241
 Db 206 QACPVKSFPPIPHTCPGTFALLCNDKNTNTKRLINGNTSVT 265
 Query 242 GSLAEFREVIRSENFTNAKTIIVQLANVSVEINCCTRPNNTTRKRVTLGPRVWTTGEI 301
 Db 266 GSLAEFDIVRSEDPTDNXKTTIVQLNESEVNCTRPNNTTRERLSIGSGRAFTARRNTI 325

Query 302 GNIRQBHCNTISRAQWNTLQOIAATTIREQGNKTIATFNQSSGGDPBEIVWHSFNCCGEFFY 361
 Db 326 GDIROQHCNTISRAKWNNTLQOIVWYKAMALPI 418
 Query 362 CNSTQLFNSAWNVT--SNGTWSVTIKQKDGTDTILPCRQIKOINRQVQKGAMALPIK 419
 Db 386 CNTAQLFNSWNVAGGTNT-----EGNDITLQCRKQIQINMWRQVKGAMALPPT 437
 Query 420 GLIRSSNTGLLTDGGGENOT-TEIFPGGMRDWRSELKYLKVYKIEPVGVAPT 478
 Db 438 GQIRSSNTGLLTDGGNSTETEIFRGGGMRDWRSELKYLKVRIEPPGVAPT 497
 Query 479 KAKRVRVQREKRAVGMGAMFLGPTGAASSTMGATSMALTYQARQLSSIVQQQNLLRA 538
 Db 498 RAKRRTVQREKRAVGC-IGAVFLGFIQAAGSTMGAASVLTVOARLILSGTVOQQNLLRA 556
 Query 539 IKAQHLLQQTWTGKQOLORILAYERLYLKQDQQLIGTWGCSKLICCTTAVPNASWSNKT 598
 Db 557 IERQNMRLRTWGIQKQARVLAERYLRDQQLMGWIGCSKLICCTTSUPNWSWSNKS 616
 Query 599 LDQIWNNTMWEDEIDNYTHLYTLLIESONQEKNOELLQDWDKASL 649
 Db 617 VDDIWNNTMWEDEIDNYTDYDLEKRSQTOBKNEKELELDKWSL 667

QY 242 GSLABEEVIRSENFTNAKTIIVQLNVSVBINGTRPNNHTRKRVTLGGGRWYTTGEI 301
 Db 266 GSLAEDIVRSDFDINVKTIVOLNESTVNCTRPNNTRERLISGRAFTARRNI 325

QY 302 GNIROAHCNISRAQVNNTLQIAITLREFGNKTAFANQSGGDPEIVNHSFNGCGEFY 361
 Db 326 GDIRQAHCNISRAQVNNTLQIVIKUREKRNKTAFAQNQSGGDPEIVNHSFNGCGEFY 385

QY 362 CNSTOLFNSAMVNT - SNGTWSVTRKQDKTDITLPCRKIQLNTRQVIATTLRBEGFGNKTAFANQSGGDPEIVNHSFNGCGEFY 361
 Db 386 CNTAQLFNSAMVNT - SNGTWSVTRKQDKTDITLPCRKIQLNTRQVIATTLRBEGFGNKTAFANQSGGDPEIVNHSFNGCGEFY 373

QY 420 GLIRCSSNITGLLITRDGGENOT - TEIIPRGDDMRDNWRSELYKVKVKEPLGVART 419
 Db 438 GQIRCSSNITGLLITRDGENSTEETEIPRGDDMRDNWRSELYKVKVKEPLGVART 425

QY 479 KAKRVRVOREKRAVGMGLGAMFLGFLGAAGSTMGAATSMALTVQARQLLSGIVQQNNLLRA 538
 Db 498 RAKRVRVOREKRAVGMGLGAMFLGFLGAAGSTMGAATSMALTVQARQLLSGIVQQNNLLRA 556

Qy 539 IKAQBLQQLLTWGIKQLOQARIЛАВЕРЛЫДQOQLGFWGCSKLICLCTAVPNNAWSNKT 598
 Db 557 IEAQNMRLLTWGIKQLOQARIЛАВЕРЛЫДQOQLGFWGCSKLICLCTAVPNNAWSNKT 616

QY 599 LDQIWNNTMNEWREIDNTYTHLYTLESQNQEBKNQELLDKMASL 649
 Db 617 VDDIWNNTMNEWREIDNTYDYLLEKSQTQEKNEKELLDKMASL 667

RESULT 6
 US-11-014-842A-29
 ; Sequence 29, Application US/11014842A
 ; Publication No. US2006001826A1

; GENERAL INFORMATION:
 ; APPLICANT: TANGY, FREDERIC
 ; APPLICANT: LORIN, CLARISSÉ
 ; APPLICANT: MOLLET, LUCILLE
 ; APPLICANT: DELEBECQUE, FREDERIC
 ; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOSES OF
 ; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
 ; FILE REFERENCE: 2356-0093
 ; CURRENT APPLICATION NUMBER: US/11/014,842A
 ; PRIORITY APPLICATION NUMBER: PCT/EP03/07146
 ; PRIOR FILING DATE: 2003-06-20
 ; PRIOR APPLICATION NUMBER: EP 02291550.8
 ; PRIOR FILING DATE: 2002-06-20
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn Ver. 3.3
 ; SEQ ID NO: 29
 ; LENGTH: 669
 ; TYPE: PRF
 ; ORGANISM: Human immunodeficiency virus type 1
 ; US-11-014-842A-29

Query Match 76.8%; Score 2668.5; DB 7; Length 669;
 Best Local Similarity 77.9%; Pred. No. 3 4e-238; Indels 33; Gaps 10;
 Matches 507; Conservative 55; Mismatches 56;

Db 206 QACPXVSFQPIPTHYCVPAGFALKCNKNDKFENGTGPCTINVSTQCTHGRPVYSTQOLLIN 265
 Qy 242 GSLLBEVVIRSENFTNAKTIIVQLNVSVBINGTRPNNHTRKRVTLGGGRWYTTGEI 301
 Db 266 GSLAEDIVRSDFDINVKTIVOLNESTVNCTRPNNTRERLISGRAFTARRNI 325
 Qy 302 GNIROAHCNISRAQVNNTLQIAITLREFGNKTAFANQSGGDPEIVNHSFNGCGEFY 361
 Db 317 ---RQAHCNISRAQVNNTLQIVIKUREKRNKTAFAQNQSGGDPEIVNHSFNGCGEFY 373
 Qy 362 CNSTOLFNSAMVNT - SNGTWSVTRKQDKTDITLPCRKIQLNTRQVIATTLRBEGFGNKTAFANQSGGDPEIVNHSFNGCGEFY 419
 Db 374 CNTAQLFNSAMVNT - SNGTWSVTRKQDKTDITLPCRKIQLNTRQVIATTLRBEGFGNKTAFANQSGGDPEIVNHSFNGCGEFY 425
 Qy 420 GLIRCSSNITGLLITRDGGENOT - TEIIPRGDDMRDNWRSELYKVKVKEPLGVART 478
 Db 426 GQIRCSSNITGLLITRDGENSTEETEIPRGDDMRDNWRSELYKVKVKEPLGVART 485
 Qy 479 KAKRVRVOREKRAVGMGLGAMFLGFLGAAGSTMGAATSMALTVQARQLLSGIVQQNNLLRA 538
 Db 486 RAKGRTVOREKRAVGMGLGAMFLGFLGAAGSTMGAATSMALTVQARQLLSGIVQQNNLLRA 556
 Qy 539 IKAQBLQQLLTWGIKQLOQARIЛАВЕРЛЫДQOQLGFWGCSKLICLCTAVPNNAWSNKT 598
 Db 545 IEAQNMRLLTWGIKQLOQARIЛАВЕРЛЫДQOQLGFWGCSKLICLCTAVPNNAWSNKT 604
 Qy 599 LDQIWNNTMNEWREIDNTYTHLYTLESQNQEBKNQELLDKMASL 649
 Db 605 VDDIWNNTMNEWREIDNTYDYLLEKSQTQEKNEKELLDKMASL 667

RESULT 7
 US-11-014-842A-31
 ; Sequence 31, Application US/11014842A
 ; Publication No. US2006001826A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TANGY, FREDERIC
 ; APPLICANT: MOLLET, LUCILLE
 ; APPLICANT: DELEBECQUE, FREDERIC
 ; APPLICANT: LORIN, CLARISSÉ
 ; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOSES OF
 ; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
 ; TITLE OF INVENTION: VACCINE COMPOSITIONS
 ; FILE REFERENCE: 2356-0093
 ; CURRENT APPLICATION NUMBER: US/11/014,842A
 ; PRIORITY APPLICATION NUMBER: PCT/EP03/07146
 ; PRIOR FILING DATE: 2004-12-20
 ; PRIOR APPLICATION NUMBER: PCT/EP03/07146
 ; PRIOR FILING DATE: 2003-06-20
 ; PRIOR APPLICATION NUMBER: EP 02291550.8
 ; PRIOR FILING DATE: 2002-06-20
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn Ver. 3.3
 ; SEQ ID NO: 31
 ; LENGTH: 857
 ; TYPE: PRF
 ; ORGANISM: Human immunodeficiency virus type 1
 ; US-11-014-842A-31

Query Match 76.8%; Score 2668.5; DB 7; Length 857;
 Best Local Similarity 77.9%; Pred. No. 4.9e-238; Mismatches 56; Indels 33; Gaps 10;

Db 3 LMVTTVYGPVWKEATTLFCASDAKAYDEAHVWATHACYPTNPNPOEVVLENTENF 62
 Db 34 LMVTTVYGPVWKEATTLFCASDAKAYDEAHVWATHACYPTNPNPOEVVLENTENF 93
 Qy 63 NMWKNNNVEQHEDIISLWDQSLKPCKVLTPLCVTLNCTDLN-TNNTNTNTELNLSIVVWE 121
 Db 94 NMWKNNNVEQHEDIISLWDQSLKPCKVLTPLCVTLNCTLNNTNTNTELNLSIVVWE 149
 Qy 122 ORGKEMRNCFSFNITTSIRDKVOREYALFYKDVDEPIDNKNTTNNTKYRLINCNTSVIT 181
 Db 150 MMEEGEIKNCFSFYITSIRNKVKKEYALFNRDVPV--KN-TSNTKYRLSCNTSVIT 205
 Qy 182 QACPXVSFQPIPTHYCVPAGFALKCNKNDKFENGTGPCTINVSTQCTHGRPVYSTQOLLIN 241

Db	150 NMEEGHIGKNCSPFYITTSIRNKVKYEAFLNRLDVVEV-- KN-TSNTKYLISCTNTSVIT 205	Qy	123 RGKGEMRNCFSNITTTSIRDKVQREYALFYKLDVREFDDNKNNTNTKYRLINCNTSVITQ 182
Qy	182 QACPYSPEPPIHYCPTGPALLKNDKFKNGTGPCTNSTVQCTHGRPVVSTOLLIN 241	Db	130 ----- NCNTSVITQ 138
Db	206 QACPYSFQPIPHYCPTGPAGFAILCKNNKTENGSPCTNSTVQCTHGRPVVSTOLLIN 265	Qy	183 ACPTYSFEPPIHYCPTGPALLKNDKFKNGTGPCTNSTVQCTHGRPVVSTOLLING 242
Qy	242 GSLAEEEVVTRSENFTNAKTTIVQLNVSIVBETCRPNHTRKRTVTLGPRWYWTGEIL 301	Db	139 ACPTYSFQPIPHYCPTGPAGFAILCKNNKTENGSPCTNSTVQCTHGRPVVSTOLLING 198
Db	266 GSLAEEDIVRSEDFTDNKTTIVQLNVSIVBETCRPNHAAEL---DKWASAA--- 316	Qy	243 SLAEEEVVTRSENFTNAKTTIVQLNVSIVBETCRPNHTRKRTVTLGPRWYWTGEIL 302
Qy	302 GNIROAHCNISRAQWNNTLQQIATTLREQFGNKTIAFNQSSGGDPEIVWHFNCGGEFFY 361	Db	199 SLAEEDIVRSEDFTDNKTTIVQLNVSIVBETCRPNHTRLUSIGPRAFYARNITG 258
Db	311 ---ROAHCNISRAQWNNTLQQIATTLREQFGNKTIAFNQSSGGDPEIVWHFNCGGEFFY 373	Qy	303 NIROAHCNISRAQWNNTLQQIATTLREQFGNKTIAFNQSSGGDPEIVWHFNCGGEFFYC 362
Qy	362 CNSTOLPNSAVNT--SNGTMSVTRKQKDIDILTPCRKQIINRNQVYQKANTALPK 419	Db	259 DIRQHCNISRAQWNNTLQQIATTLREQFGNKTIAFNQSSGGDPEIVWHFNCGGEFFYC 318
Db	374 CNTAQLFNSTVNAGGTGT-----EGNDITLTCRQIKQTINMWQKVGMAYAPPIT 425	Qy	363 NSTQFNSAMVNT--SNGTMSVTRKQKDIDILTPCRKQIINRNQVYQKANTALPKG 420
Qy	420 GLIRCSSNITGLLITRDGGENQT-TBIFRGGDMDNRVSELTYKVKRIEPVGAPIT 478	Db	319 NTQALFNSTVNAGGTGT-----EGNDITLTCRQIKQTINMWQKVGMAYAPPITG 370
Db	426 GQIRCSSNITGLLITRDGGNSTETETEFRGGDMDNRVSELTYKVKRIEPVGAPIT 485	Qy	421 LIRCSSNITGLLITRDGGENOT-TBIFRGGGDMDRDNVSELTYKVKRIEPVGAPIT 479
Qy	479 KAKRRTVQREKRAVGMGLGAMPFLGFLGAAGSTMGATSMALTYQARQLSGIVQOQNLLRA 538	Db	371 QIRCSSNITGLLITRDGGNSTETETEFRGGDMDNRVSELTYKVKRIEPVGAPIT 430
Db	486 RAKRRTVQREKRAVGMGLGAMPFLGFLGAAGSTMGAASVTLTYQARQLSGIVQOQNLLRA 544	Qy	480 AKRRTVQREKRAVGMGLGAMPFLGFLGAAGSTMGATSMALTYQARQLSGIVQOQNLLRAI 539
Qy	539 IKAQHILLQLTWGIGOLQARIЛАВЕРЛУДОQLLGFWGSGSKLICCTAВРННАСWSNCT 598	Db	431 AKRRTVQREKRAVGMGLGAMPFLGFLGAAGSTMGAASVTLTYQARQLSGIVQOQNLLRAI 489
Db	545 IEAQQMLRLTWGIGOLQARIЛАВЕРЛУДОQLLGFWGSGSKLICCTAВРННАСWSNKS 604	Qy	540 KAQQHILLQLTWGIGOLQARIЛАВЕРЛУДОQLLGFWGSGSKLICCTAВРННАСWSNKL 599
Qy	599 LDQIWNMNTMNEWDRBDNTNTHLYTLLTIEESQNOQEKNQOBLLQDQKWL 649	Db	490 EAQQMLRLTWGIGOLQARIЛАВЕРЛУДОQLMGFWGSGSKLICCTAВРННАСWSNKS 649
Db	605 VDDIWNMNTMNEWEREIDNTDYLLEXSTQDQRNEBELLELDKWL 655	Qy	600 DQIWNMNTMNEWDRBDNTNTHLYTLLTIEESQNOQEKNQOBLLQDQKWL 649
Db		550 DDIWNMNTMNEWEREIDNTDYLLEXSTQDQRNEBELLELDKWL 599	
RESULT 8			
; Sequence 33, Application US/11014842A			
; Publication No. US2006001386A1			
; GENERAL INFORMATION:			
; APPLICANT: TANGY, FREDERIC			
; APPLICANT: LORIN, CLARISSE			
; APPLICANT: MOLLET, LUCILE			
; APPLICANT: DELERQUE, FREDERIC			
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOSES OF			
; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF			
; FILE REFERENCE: 2356-0093			
; CURRENT APPLICATION NUMBER: US/11/014,842A			
; CURRENT FILING DATE: 2004-12-20			
; PRIOR APPLICATION NUMBER: PCT/EP03/07146			
; PRIOR FILING DATE: 2003-06-20			
; PRIOR FILING DATE: 2002-06-20			
; NUMBER OF SEQ ID NOS: 43			
; SOFTWARE: PatentIn Ver. 3.3			
; SEQ ID NO: 33			
; LENGTH: 613			
; TYPE: PRT			
; ORGANISM: Human immunodeficiency virus type 1			
; US-11-014-842A-33			
; Sequence 33, Application US/11014842A			
; Publication No. US2006001386A1			
; Sequence 35, Application US/11014842A			
; Publication No. US2006001386A1			
; GENERAL INFORMATION:			
; APPLICANT: TANGY, FREDERIC			
; APPLICANT: LORIN, CLARISSE			
; APPLICANT: MOLLET, LUCILE			
; APPLICANT: DELERQUE, FREDERIC			
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOSES OF			
; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF			
; FILE REFERENCE: 2356-0093			
; CURRENT APPLICATION NUMBER: US/11/014,842A			
; CURRENT FILING DATE: 2004-12-20			
; PRIOR APPLICATION NUMBER: PCT/EP03/07146			
; PRIOR FILING DATE: 2003-06-20			
; NUMBER OF SEQ ID NOS: 43			
; SOFTWARE: PatentIn Ver. 3.3			
; SEQ ID NO: 35			
; LENGTH: 801			
; TYPE: PRT			
; ORGANISM: Human immunodeficiency virus type 1			
; US-11-014-842A-35			
; Query Match Score 2509.5; DB 7; Length 613;			
; Best Local Similarity 72.6%; Pred. No. 1.5e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5; DB 7; Length 801;			
; Best Local Similarity 72.6%; Pred. No. 2.1e-223; Indels 87; Gaps 5;			
; Matches 472; Conservative 49; Mismatches 42; Gaps 87;			
; Query Match Score 2509.5			

QY 63 NMWKNMVEQMHEIDISLWDOSLKPCVKUTPLCYTLNCIDLNNTNTTELSIVVWEQ 122
 Db 94 NMWKNMVDNHEIDISLWDOSLKPCVKUTPLCYTLNCIDLNNTNTTELSIVVWEQ 129
 QY 123 RGKGMEMRNCFSNITTSIRDKVOREVALFYKLDVEPIDDNKNTNTKCLINCNTSVITQ 182
 Db 130 -----NCNTSVITQ 138
 Qy 183 ACPKVSFEPIPHYCPTGPFALLKCNKDFCKENGTGBCTNVSTVOCTHIGRPVSTOLLING 242
 Db 139 ACPKVSFQPPIHYCPTGPFALLKCNKTFNGSPTCNVSTVOCTHIGRPVSTOLLING 198
 QY 243 SLAERBVVRSERNFTNAKTLIVOLNVSEINCTRPNHNTKRKVTLGPGRWYTGEIL 302
 Db 199 SLAEDIVRSERDFTDVNLIVOLNVSEINCTRPNHNTTRERUSIGPRAFARRNG 258
 QY 303 NIROAHCNISRAQWNTLLOQATTLREQGKNTIAFPNQSGGDEPEIWMESFCGGEFFYC 362
 Db 259 DIROAHCNISRAKWNTLLOQIVIKREKRFNKTAIAFNQSGGDEPEIWMESFCGGEFFYC 318
 Qy 363 NSTQLENSAWNTT-SNGTWSVTQRQKDGTIDITLPCRIKIQIINRMQVKAMYALPIK 420
 Db 319 NTAQLENSAWNTT-BGNDITLQCRKQIINRMQVKAMYALPIK 420
 Qy 421 LIRCSSNTGGLTRDGGGENOT-TBIFPGGDMRDNRWSELKYKVKIEPIGVAPTK 479
 Db 371 QIRCSSNTGGLTRDGGNSTETEIPFGGDMRDNRWSELKYKVKIEPIGVAPTK 430
 Qy 480 AKRRTVQERKRAVGMLGANFLGFLGAAGSTMAGTSMALTQAROLLSVGQQNNLLRAI 539
 Db 4331 AKRRTVQERKRAVG-IGAVFLGFLGAAGSTMAGASVLTQARNLSSVGQQNNLLRAI 489
 Qy 540 KAQQLLQLQJTWGKIKOLQARILAYERYLKDDQQLLGFWGCSGKLICITAVPNASWSNKL 599
 Db 490 EAQQNMLRLTWGKIKOLQARILAYERYLDDQQLLGFWGCSGKLICITAVPNASWSNKL 549
 Qy 600 DQIWNNMWMDREIDNTTHLTLTIESQNQEKNOELLDKWL 649
 Db 550 DDIWNNMWMDREIDNTDYDLDLESQTKQEKENELLDKWL 599
 QY 62 FMMKQNMVEQMHEIDISLWDOSLKPCVKUTPLCYTLNCIDLNNTNTTELSIVVWE 121
 Db 92 NMWKNMVDNHEIDISLWDOSLKPCVKUTPLCYTLNCIDLNNTNTTELSIVVWE 147
 QY 122 QRKGKEMRNCFSNITTSIRDKVOREVALFYKLDVEPIDDNKNTNTKCLINCNTSVIT 181
 Db 148 NNNTSDMNCFSNATETTDKIRKENALFYTDIVPDENQ--NNSYRNLNCNTSKV 204
 QY 182 QACPKVSFERPIPHYCTPTGFALLKCNKDFCKENGTGBCTNVSTVOCTHIGRPVSTOLLING 241
 Db 205 QACPKVSFDPIPHYCAPAGYATLCKCNNTFNGTGPVNVSITQCTGKIPKVSTOLLING 264
 QY 242 GSLAEEVIRSENFTNAKTLIVOLNVSEINCTRPNHNTTRKVTLGPGRWYTGEIL 301
 Db 265 GSRAKEETIRSRMNTNAKTLIVOLNVSEINCTRPNHNTTRKVTLGPGRWYTGEIL 324
 QY 302 GNFRQHRCNTISRAQWNTLLOQATTLREQGKNTIAFPNQSGGDEPEIWMHESFCGGEFFY 361
 Db 325 GDRQAHCNISGADWNRLTQGVCRKLAGYFPNKTISFOPSSGCDLEITHSFCNGEFFY 384
 QY 362 CNSQLENSAWNTT-SNGTWSVTQRQKDGTIDITLPCRIKIQIINRMQVKAMYALPIK 419
 Db 385 CNTSSLFNTTYRTPWNGT-----BSNSTTLCRIKIQIINRMQVKAMYALPIK 436
 QY 420 GLIRCSSNTGGLTRDGG - GGBNQTEBEIPRGGDMRDNRWSELKYKVKIEPIGVAP 477
 Db 437 GKTCNSNTGGLTRDGGNTTBEIPRGGDMRDNRWSELKYKVKIEPIGVAP 496
 Qy 478 TRAKRRTVQERKRAVGMLGANFLGFLGAAGSTMAGTSMALTQAROLLSVGQQNNLLRAI 537
 Db 497 TGAKRRTVQERKRAVG-IGAVFLGFLGAAGSTMAGASVLTQARNLSSVGQQNNLLRAI 555
 Qy 538 ATKAQQLLQLQJTWGKIKOLQARILAYERYLKDDQQLLGFWGCSGKLICITAVPNASWSNKL 597
 Db 556 ATEQQHHLQLLTWGKIKOLQARILAYERYLDDQQLLGFWGCSGKLICITAVPNASWSNKL 615
 QY 598 TLDQIWNNMWMDREIDNTTHLTLTIESQNQEKNOELLDKWL 649
 Db 616 SQADWDNTNWMDREISNTDTYRALLEVSQDQNEQDILANKWHL 667

RESULT 11

US-11-014-842A-37
 Sequence 37, Application US/11014842A
 ; Publication No. US20060013826A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tangy, Frederic
 ; APPLICANT: Lorin, Clarisse
 ; APPLICANT: Mollet, Lucile
 ; APPLICANT: Delebreque, Frederic
 ; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPEs OF
 ; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
 ; FILE REFERENCE: 2356-0093
 ; CURRENT APPLICATION NUMBER: US/11/014-842A
 ; TITLE OF INVENTION: VACCINE COMPOSITIONS
 ; FILE REFERENCE: 2356-0093
 ; CURRENT FILING DATE: 2004-12-20
 ; PRIOR APPLICATION NUMBER: PCT/EP03/07146
 ; PRIOR FILING DATE: 2003-06-20
 ; PRIOR APPLICATION NUMBER: EP 02291550.8
 ; PRIOR FILING DATE: 2002-06-20
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn Ver. 3.3
 ; SEQ ID NO: 37
 ; LENGTH: 601
 ; ORGANISM: Human immunodeficiency virus type 1
 ; Query Match Score 2421.5; DB 7; Length 601;
 ; Best Local Similarity 71.1%; Pred. No. 1.9e-215;
 ; Matches 44; Conservative 44; Mismatches 45; Indels 99; Gaps 7;
 ; US-11-014-842A-37
 QY 3 LMVTVYYGVPVWKEAATTLFCAKTDAYDTEAHNVWATHACVPTNPQEVVLENNTENF 62

Db 34 LWTVYGGPVWREACTLFCASDAYDAYDTEVNYWATHACVPTDNPQEVTGLNVTNF 93
 Qy 63 NWKRNNEQMEEDIISLWDQSLLKPCVTRLPCVTCVNTCTDLNTNNNTTBLSTLSIIVVWEQ 122
 Db 94 NWKRNNDQMEEDIISLWDSESLKPCVTRLPCVTL ------ 129
 Qy 123 RGKGMEMNCFSNITTSIRDKYQREYALFYKLDVPERDDNKNTTNTKYLINCNTSVTQ 182
 Db 130 -----
 Qy 131 -----
 Db 132 -----
 Qy 133 ACPKVSPBPIPHYCPTGPALKCNDKKGKNGTGPCTNVSTVQCTHGRIPVUSTOLLING 242
 Db 139 ACPKVSPBPIPHYCPTGPALKCNDKKGKNGTGPCTNVSTVQCTHGRIPVUSTOLLING 198
 Qy 243 SLAEEETVIRSENFTNMAKTTIVQLNVSVEINCTRPNHTRKRTVLGPRWYTGTBLG 302
 Db 199 SLAEEETVIRSENFTNMAKTTIVQLNVSVEINCTRPNHTRKRTVLGPRWYTGTBLG 302
 Qy 303 NIROAHCNISRAQWNNTLQQIAUTTLEQFGNKTAIFNQSSGDPBEVMSFNCGGEFFYC 362
 Db 249 --RQAHENISRAKWANTLQQIVTKLERFRNKTAIANQSSGDPETVMSFNCGGEFFYC 306
 Qy 363 NSTOLENSAWNT-SNGTWSVTRKQDITLPCRKOIQINRQVKGAMYALPIKG 420
 Db 307 NTAQLENSTWAVGNT-----EGNDITLQCRKQTINMVKQVKAMYAPPITG 358
 Qy 421 LIRCSSNTIGLLTRDGGENOT-TEIFRPGGDMRDNRSELVYKVVIEPLGVAPTR 479
 Db 359 QIRCSSNTIGLLTRDGGSNTETETEFRPGGDMRDNRSELVYKVVIEPLGVAPTR 418
 Qy 480 AKRRVYQREKZAVGMILGAMFLGFLGAAGSTMGATSNVALTYQAROLISGTVQQNNLLRAI 539
 Db 419 AKRRVYQREKZAVGMILGAMFLGFLGAAGSTMGAASVTLTYQAROLISGTVQQNNLLRAI 477
 Qy 540 KAQQHLLQLTWGIQKOLQARILAVERYLKDQQLLGAGSTMGAASVTLTYQAROLISGTVQQNNLLRAI 539
 Db 478 EAQQNMLRLTWGIQKOLQARILAVERYLKDQQLLGAGSTMGAASVTLTYQAROLISGTVQQNNLLRAI 477
 Qy 541 DQINNMNTWWEDRBDNTTHLYTLEESQNQOKNOELLOLDKWASL 649
 Db 538 DDINNMNTWWEREDNTDYDYLLEKSQTQERNEKEELLDKWASL 587
 RESULT 12
 US-11-014-842A-39
 Sequence 39, Application US/11014842A
 Publication No. US20060013826A1
 GENERAL INFORMATION:
 APPLICANT: TANGY, FREDERIC
 APPLICANT: LORIN, CLARISSÉ
 APPLICANT: DELERQUE, FREDERIC
 APPLICANT: MOLLET, LUCILE
 TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPE OF
 TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
 TITLE OF INVENTION: VACCINE COMPOSITIONS
 FILE REFERENCE: 2356.0093
 CURRENT APPLICATION NUMBER: US/11/014842A
 CURRENT FILING DATE: 2004-12-20
 PRIOR APPLICATION NUMBER: PCT/EP03/07146
 PRIOR FILING DATE: 2003-06-20
 PRIOR APPLICATION NUMBER: EP 02291550.8
 PRIOR FILING DATE: 2002-06-20
 SOFTWARE: PatentIn Ver. 3.3
 SEQ ID NO 39
 LENGTH: 789
 TYPE: PRT
 ORGANISM: Human immunodeficiency virus type 1
 US-11-014-842A-39
 Query Match 69.7%; Score 2421.5; DB 7; Length 789;
 Best Local Similarity 71.1%; Pred. No. 2.8e-215; Pred. No. 7.2e-97; Length 879;

Matches 462; Conservative 44; Mismatches 45; Indels 99; Gaps 7;
 Qy 3 LWVTTYGYPWKETATTLCASDAKAYDTEBAHNWATHACVPTPNPQEVTGLNVTNF 62
 Db 34 LWVTTYGYPWKETATTLCASDAKAYDTEBAHNWATHACVPTPNPQEVTGLNVTNF 93
 Qy 63 NMWKNMVEQNHEDISLWDOSLKEPCVKGTPLCVTLNCTDLNTNNNTNTBLSTLSIIVVWEQ 122
 Db 94 NMWKNMVDQMEEDIISLWDSESLKPCVKGTPLCVTL ------ 129
 Db 123 RGKGMEMNCFSNITTSIRDKYQREYALFYKLDVPERDDNKNTTNTKYLINCNTSVTQ 182
 Db 130 -----
 Qy 183 ACPKVSPBPIPHYCPTGPALKCNDKKGKNGTGPCTNVSTVQCTHGRIPVUSTOLLING 242
 Db 139 ACPKVSPBPIPHYCPTGPALKCNDKKGKNGTGPCTNVSTVQCTHGRIPVUSTOLLING 198
 Qy 243 SLAEEETVIRSENFTNMAKTTIVQLNVSVEINCTRPNHTRKRTVLGPRWYTGTBLG 302
 Db 199 SLAEEETVIRSENFTNMAKTTIVQLNVSVEINCTRPNHTRKRTVLGPRWYTGTBLG 302
 Db 199 SLAEDIVRSDFDNKVTIVQLNESVVINCTRPNNAEL-----DKWASA-----DKWASA-----248
 Db 249 --RQAHENISRAKWANTLQQIVTKLERFRNKTAIANQSSGDPETVMSFNCGGEFFYC 306
 Qy 303 NIROAHCNISRAQWNNTLQQIAUTTLEQFGNKTAIFNQSSGDPB1VMSFNCGGEFFYC 362
 Db 249 --RQAHCNISRAKWNNTLQQIVKIREKFKNKTAIFNQSSGDPB1VMSFNCGGEFFYC 306
 Qy 363 NSTQFNSANVNT-SNGTWSVTRKQDITLPCRKOIQINRQVKGAMYALPIKG 420
 Db 307 NTAQLENSTWAVGNT-----EGNDITLQCRKQTINMVKQVKAMYAPPITG 358
 Qy 421 LIRCSSNTIGLLTRDGGENOT-TEIFRPGGDMRDNRSELVYKVVIEPLGVAPTR 479
 Db 359 QIRCSSNTIGLLTRDGGSNTETETEFRPGGDMRDNRSELVYKVVIEPLGVAPTR 418
 Qy 480 KAQQHLLQLTWGIQKOLQARILAVERYLKDQQLLGAGSTMGAASVTLTYQAROLISGTVQQNNLLRAI 539
 Db 478 EAQQNMLRLTWGIQKOLQARILAVERYLKDQQLLGAGSTMGAASVTLTYQAROLISGTVQQNNLLRAI 477
 Qy 540 KAQQHLLQLTWGIQKOLQARILAVERYLKDQQLLGAGSTMGAASVTLTYQAROLISGTVQQNNLLRAI 539
 Db 600 DQINNMNTWWEDRBDNTTHLYTLEESQNQOKNOELLOLDKWASL 649
 Db 538 DDINNMNTWWEREDNTDYDYLLEKSQTQERNEKEELLDKWASL 587
 RESULT 13
 US-11-022-562-340
 Sequence 340, Application US/11022562
 Publication No. US20050249742A1
 GENERAL INFORMATION:
 APPLICANT: Ruprecht, Ruth M.
 APPLICANT: Shisong, Jiang
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
 A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
 FILE REFERENCE: DFN-043CN
 CURRENT APPLICATION NUMBER: US/11/022,562
 CURRENT FILING DATE: 2004-12-22
 PRIOR APPLICATION NUMBER: PCT/US03/20322
 PRIOR FILING DATE: 2003-06-27
 PRIOR APPLICATION NUMBER: 60/3922718
 PRIOR FILING DATE: 2002-06-27
 SOFTWARE: FastSEQ for Windows Version 4.0
 NUMBER OF SEQ ID NOS: 340
 SEQ ID NO 340
 LENGTH: 879
 TYPE: PRT
 ORGANISM: Simian Immunodeficiency Virus
 US-11-022-562-340

ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/084,858
FILING DATE: 21-Mar-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/000,321
FILING DATE: 04-Dec-2001
APPLICATION NUMBER: 09/131,551
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 58315/106/BBAK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-11-084-858-11

Query Match 18.8%; Score 653; DB 7; Length 145;
Best Local Similarity 87.3%; Pred. No. 5.2e-53;
Matches 119; Conservative 13; Mismatches 4; Indels 0; Gaps 0;
Qy 514 SMALTYQRQLSGLTIVQQQNLLRAIKAQQLLQLTVWGIKQLQARILAVERYLKDQQL 573
Db 2 SILTIVQRQLSGLTIVQQQNLLRAEQQLLQLTVWGIKQLQARILAVERYLKDQQL 61
Qy 574 GFWGCSGKLLCTTAVPNASNSNKTLDQIWNNTWWMEWDREIDNYTHLYTLLBESQNQQ 633
Db 62 GIWGCSGKLLCTTAVPNASNSNKSLEDIWNNTWWMEWDREIDNYTNTYTLBESQNQQ 121
Qy 634 EKNOQELLQDKWASL 649
Db 122 EKNEQELLEDQDKWASL 137

Search completed: March 7, 2006, 17:57:10
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